

86691

Delaval, Jan

From: Gambel, Phillip
Sent: Thursday, February 13, 2003 9:52 AM
To: Delaval, Jan
Subject: 09 / 425516 freeman amd

jan

please perform a sequence and a sequence interference search for

usssn 09 / 425,516 (freeman amd)

SEQ ID NO: 2

SEQ ID NO: 23

thanx

phillip gambel
art unit1644
308-3997

Room 8B83

1644 mailbox 9e12

if by chance, you have done this recently,
please print out

this case was removed from my office and i don't see an updated sequence in the case
thanx

Jan Delaval
Reference Librarian
Biotechnology & Chemical Library
C411 1E07 - 703-303-4498
jan.delaval@uspto.gov

08/452210

BioTech-Chem Library

Search Results

Feedback Form (Optional)



Scientific & Technical Information Center

The search results generated for your recent request are attached. If you have any questions or comments (compliments or complaints) about the scope or the results of the search, please contact *the BioTech-Chem searcher* who conducted the search *or contact*:

Mary Hale, Supervisor, 308-4258
CM-1 Room 1E01

Voluntary Results Feedback Form

➤ *I am an examiner in Workgroup:* (Example: 1610)

➤ *Relevant prior art **found**, search results used as follows:*

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ *Relevant prior art **not found**:*

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Search results were not useful in determining patentability or understanding the invention.

Other Comments:

Drop off completed forms at the **Circulation Desk CM-1**, or send to Mary Hale, CM1-1E01 or e-mail mary.hale@uspto.gov.

GenCode version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 13, 2003, 11:29:24 ; Search time 15.4702 seconds

(without alignments)
2044.459 Million cell updates/sec

Title: US-09-425-516-2

Perfect score: 1733

Sequence: 1 HQPQVTWMLNLPWAFIL.....AQRVFSSTKCKNDITCF 329

Scoring table: BLOSUM62

Gapop 10.0 , Gapexc 0.5

Searched: 283224 seqs, 9613442 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Display first 45 summaries

Database : PIR 73:*

1: P113:*

2: P112:*

3: P113:*

4: P114:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1733	99.9	325	2	CD86 precursor - r
2	1384	79.9	275	2	CD86 precursor - r
3	963.5	55.6	330	2	CD86 precursor - r
4	785.2	43.2	109	2	CD86 precursor - r
5	752.2	41.2	109	2	CD86 precursor - r
6	243	14.0	299	2	CD80 precursor - r
7	243	14.0	309	2	CD80 precursor - r
8	243	14.0	309	2	B-lymphocyte activ
9	201.5	11.6	288	2	B-cell-restricted
10	187.5	10.8	289	2	B7 protein - red-c
11	187.5	10.8	289	2	B7 protein - red-c
12	187.5	10.8	289	2	B7 protein - red-c
13	187.5	10.8	289	2	B7 protein - red-c
14	187.5	10.8	289	2	B7 protein - red-c
15	187.5	10.8	289	2	B7 protein - red-c
16	187.5	10.8	289	2	B7 protein - red-c
17	187.5	10.8	289	2	B7 protein - red-c
18	187.5	10.8	289	2	B7 protein - red-c
19	187.5	10.8	289	2	B7 protein - red-c
20	187.5	10.8	289	2	B7 protein - red-c
21	187.5	10.8	289	2	B7 protein - red-c
22	187.5	10.8	289	2	B7 protein - red-c
23	187.5	10.8	289	2	B7 protein - red-c
24	187.5	10.8	289	2	B7 protein - red-c
25	187.5	10.8	289	2	B7 protein - red-c
26	187.5	10.8	289	2	B7 protein - red-c
27	187.5	10.8	289	2	B7 protein - red-c
28	187.5	10.8	289	2	B7 protein - red-c
29	187.5	10.8	289	2	B7 protein - red-c
30	187.5	10.8	289	2	B7 protein - red-c

ALIGNMENTS

RESULT 1

A:Query: B7-2 antigen - human	30	104.5	6.0	5198	2	744290	hesicentin precursor
A:Residues: 1-139	31	104	6.0	292	2	744230	hypothetical prote
A:Score: 1733	32	103	5.9	871	1	148696	protein-tyrosine k
A:Cross-references: CB12259; NID:G416368; PID:AA58388.1; PID:G416369	33	103	5.9	871	1	148696	protein-tyrosine k
A:Map position: 3q13.3-q21	34	102.5	5.9	991	2	G87723	protein RGA10.4 f
A:Keywords: glycoprotein	35	102	5.9	931	2	G87723	protein RGA10.4 f
A:Title: Cloning of B7-3, a CTLA-4 counter-receptor that costimulates human T cell prol	36	101.5	5.9	789	2	G18642	hypothetical prote
A:Residues: 1-139	37	101	5.9	789	2	G18642	hypothetical prote
A:Score: 1733	38	101	5.8	147	2	G18642	hypothetical prote
A:Cross-references: CB12259; NID:G416368; PID:AA58388.1; PID:G416369	39	101	5.8	1274	2	G18642	hypothetical prote
A:Map position: 3q13.3-q21	40	100.5	5.7	570	2	A57535	neuroxin type F
A:Keywords: glycoprotein	41	99.5	5.7	570	2	A57535	neuroxin type F
A:Title: Cloning of B7-3, a CTLA-4 counter-receptor that costimulates human T cell prol	42	98.5	5.7	941	1	TWWD	protein-tyrosine k
A:Residues: 1-139	43	98	5.7	941	1	TWWD	protein-tyrosine k
A:Score: 1733	44	98	5.7	668	2	G53356	hypothetical prote
A:Cross-references: CB12259; NID:G416368; PID:AA58388.1; PID:G416369	45	97.5	5.6	285	2	G36903	PC gamma 1(GC) rec

Oy 184 GIMOK-----SQNVTELVDSLSVSPVSTNTFCLETCKTLLASILEED 238
 Oy 180 GELAAIDTTSVQVETLTIVSSLDQ-----NTRFNSVCLVYGLVLA-VQNTNNTK 235
 Oy 239 POPPPIIT--PW-----ITNVLPITVTCVWFLCMLLWKKKPKSPNSKYGTNTMEER 290
 Db 236 GCHFTNLLSSNLTSLWGVICVLCYCF-----APCRSENNELABE 283
 RESULT 11
 565113
 butyrophilin - mouse (fragment)
 C-Date: 13-Mar-1997 #sequence_revision 13-Mar-1997 #text_change 05-Nov-1999
 Accession: S65113 N. Noda, R. Adachi, T. Nakamura, R. Matsuda, T.
 Biochim. Biophys. Acta 1245, 286-292, 1995.
 A-Title: Carboxy-terminal cytoplasmic domain of mouse butyrophilin specifically associates with the transmembrane protein
 A-Accession: S65113 PMID: 86125722; PMID: 8511302
 A-Status: preliminary
 A-Molecule type: mRNA
 A-Keywords: transmembrane protein
 A-Cross-references: GI:80442; NID: g1246078; PID: AAB35493.1; PID: g1246079
 Query Match 10.41; Score 173.5; DB 2; Length 487;
 Best Local Similarity 26.14; Pred. No. 0.0022;
 Matches 73; Conservative 49; Mismatch 12; Indels 3; Gaps 13;
 Oy 33 NTRAPLQCFSPNSQNSGLSELYVQQRNUNLNFVPL-CHKEFDVSNKYGTSPED 91
 Db 7 SDAALDTQFSPNSQNSGLSELYVQQRNUNLNFVPL-LYRQDQEQRTQRTGATLATA 64
 Oy 92 SN-----TLRLNLIQIKKGLVQCIHKKKTQHTHOMSELSVLANFQEPVPSN 146
 Db 65 GLQDQRTLTLDVDFQCFQTCFLQDDQDEAVY-----LKVANGSDQI--SMT 117
 Oy 147 ITENVINLNCISLHYPFKQNSVLRLTKNSTEYDGIHOMSQNVTELVDSLSVS 206
 Db 118 VQGNQNSGLSELYVQQRNUNLNFVPL-CHKEFDVSNKYGTSPED 173
 Oy 207 FQVTSMTFTFLETKTLLASILEEDDQD-PPSHITVITVFLVTCVWFLC 265
 Db 174 DSSI-KNNSC-CL-----QNLTLQCKQVHLSUPHPTVLTAVLV-AIILALQDT 225
 Oy 266 ----ILWKKKKQSPNSKYGTNTMEERSESDTKREKH 302
 Db 226 IGSITFTMLYERSHSGKNSERKSLRLELCKRTKLVH 265
 RESULT 12
 570597
 butyrophilin precursor - human
 C-Date: 11-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jul-2000
 Accession: S70597 N. Noda, R. Adachi, R. L. Colico, J. R.
 Biochim. Biophys. Acta 1306, 1-1996
 A-Title: Cloning and sequence analysis of human butyrophilin reveals a potential receptor
 A-Accession: S70597 PMID: 9620169; PMID: 8616164
 A-Status: preliminary
 A-Molecule type: mRNA
 A-Keywords: transmembrane protein
 A-Cross-references: EMBL: U9576; NID: g1246082; PID: AACS0449.1; PID: g1246083
 Query Match 0.41; Score 167; DB 2; Length 526;
 Best Local Similarity 23.31; Pred. No. 9.26;
 Matches 83; Conservative 57; Mismatch 156; Indels 52; Gaps 17;
 Oy 3 PCHWNLNLTFLWFLLEG-----APRLQATFNTEFLQCFSPNSQNSGLSELYV 57

Db 10 PCLLTLL--ILLQIKLQUSAPFOVGPPEPLVAVGDELBELPCL--SNAGSHLELW 65
 Oy 58 QDENLVNELYL--GKEFDVSNKYGTSPEDS-----HTLRNLIQIKKGLVQ 109
 Db 66 FRUK--VSPAVVHQBDEQAEQVETGATLVQDLAGVALLTGVVSDGET 123
 Oy 114 CTHHKKPTQHTHOMSELSVLANFQEPVPSNTFCLETCKTLLASILEED 169
 Db 123 CYFFQDSEYEALVH-----LKVALLGSDRI--SNQVDSGLCETSVQVTEPQ-- 174
 Oy 170 SVLPSTQSTLEFDQIKQNSQNVTELVDSLSVSPVSTNTFCLETCKTLLAS 229
 Db 175 -VQRTTQSGE-KFPTSESNRSDDEGLFTVAASVTLR--DSTNSQVYIC--NLLG 326
 Oy 210 SPFSLSELDQD-PPSHITVITV-LPVTVCVWFLCMLWKK-----KKFSPNSKYG 283
 Db 227 QEKVYKITPSSGLRTPVAVAVLMLGLQIGISFTFMYLNEPREDNF----- 283
 Oy 284 TNMERESESDTKREKH-----PERSDAQRVSNKYGTSCDS 325
 Db 284 -SREKCLLELKKRATLAVDVTDTAPHLFVDSNSVLEDS 330
 RESULT 13
 A17921
 butyrophilin - bovine
 C-Species: Bos primigenius taurus (cattle)
 C-Accession: A17921 #sequence_revision 30-Apr-1991 #text_change 05-Nov-1999
 R-Jack, L.J.W.; Mather, I.H.
 J. Biol. Chem. 265, 14483-14486, 1990
 A-Title: Cloning and analysis of a cDNA encoding bovine butyrophilin, an apical glycoprotein
 A-Accession: A17921 PMID: 90354441; PMID: 2387867
 A-Reference number: A17921; NID: g1763685; PID: AAB39766.1; PID: g142773
 A-Molecule type: mRNA
 A-Status: preliminary
 A-Cross-references: GI:815551; NID: g1763685; PID: AAB39766.1; PID: g142773
 C-Keywords: transmembrane protein
 Query Match 9.31; Score 152; DB 2; Length 526;
 Best Local Similarity 23.01; Pred. No. 0.0022;
 Matches 80; Conservative 61; Mismatch 155; Indels 52; Gaps 16;
 Oy 5 CTVGLSNTLPVNFELSGAPL-----KQAVNTADQLQSPNSQNSGLSELYV 57
 Db 8 CIACCLLFIILQLQKLSAPFOVGPPEPLVAVGDELBELPCL--SPNSAGHLELW 65
 Oy 58 QDENLVNELYL--GKEFDVSNKYGTSPEDS-----SMTLRNLIQIKKGLVQ 109
 Db 66 FRUK--VSPAVVHQBDEQAEQVETGATLVQDLAGVALLTGVVSDGET 123
 Oy 110 CTHHKKPTQHTHOMSELSVLANFQEPVPSNTFCLETCKTLLASILEED 169
 Db 123 CYFFQDSEYEALVH-----LKVALLGSDRI--SNQVDSGLCETSVQVTEPQ-- 174
 Oy 170 SVLPSTQSTLEFDQIKQNSQNVTELVDSLSVSPVSTNTFCLETCKTLLAS 229
 Db 175 -VQRTTQSGE-KFPTSESNRSDDEGLFTVAASVTLR--DSTNSQVYIC--NLLG 326
 Oy 210 SPFSLSELDQD-PPSHITVITV-LPVTVCVWFLCMLWKK-----KKFSPNSKYG 283
 Db 227 QEKVYKITPSSGLRTPVAVAVLMLGLQIGISFTFMYLNEPREDNF----- 283
 Oy 284 TNMERESESDTKREKH-----PERSDAQRVSNKYGTSCDS 325
 Db 284 -SREKCLLELKKRATLAVDVTDTAPHLFVDSNSVLEDS 330
 RESULT 14
 J67780
 consensin and adenosine receptor - bovine

C.Species: Bos grunniens (cattle)
 C.Date: 02-Apr-2002 Sequence revision 02-Apr-2002 #ext_change 11-May-2000
 C.Accession: J27780
 C.Description: B. keyaerts, E. J. Lubbers, M. Van Rens, M. Boudry, R. Boudry, C. Van Rens, G. S. 2002
 A.Title: Characterization of a cDNA encoding the bovine coxsackie and adenovirus receptor
 A.Reference number: J27780
 A.Accession: J27780
 A.Molecule type: mRNA
 A.Date: 1998-01-01
 A.Creation services: CHAY01651
 C.Comment: This protein serves as the primary adenoviral attachment site on bovine cells

Query Match
 Best Local Similarity 21.3%; Pred. No. 0.011;
 Matches 86; Conservative 46; Mismatches 109; Indels 110; Gaps 20;

Qy 13 LPFVALLSGAPL-----KIAVFETALDQPF-----ANS 45
 Db 3 LLLPFLAGVADPTGSLSTTPETKAKSTALCTCTGPGDQPLDEWLLSRA 62
 Qy 46 QNQLSELVPMQDQVNLVLEKNEKTSVSKYKWTSGPDSN-----TLRLNL 100
 Db 63 DKNQVQV-----LQSGKTDYDQVGHVFTSGLKSGDASVNLG 110
 Qy 101 QKQKGLVQCIHQKPTQMRHOMSELSVLANFSGEIVPENTENYIN-----154
 Db 111 QLSQDGVQGV-KAAG-VGNKKGLQTV-----VWESG-SCYVSGSEIG 155
 Qy 155 -----ITCSHGTPKPMKSVILATNTSTYKCIQKMSQNVLTQVLSLSVST-PO 209
 Db 156 NQFLKAC-----EKESGLPTA--YE-WKLSH-----SQKLPSTLPE 191
 Qy 210 VTSN-----TIFCLSTKTRLLSGPFSLELPDPPPHIPIWT-----AV 232
 Db 192 MTSPIVSNKASAEYGTTC--TVNRSQDCLLRL-DVYFNSNAGTACAVIGTL 247
 Qy 253 LPTVILCWVFCILLANKKKKRPNSKYQNTNMRSESSQTKBKXIHPESSDAQR 312
 Db 248 LALLVALILVFC-----HKQREKY-----EKGVHDIREDVPPKSTSTAR 292
 Qy 313 VFKSEKSS 321
 Db 293 STGNSNS 301

RESUR 15
 Tractin - medicinal leech
 C.Species: Hirudo medicinalis (medicinal leech)
 C.Date: 02-Apr-2002 Sequence revision 15-Oct-1999 #ext_change 11-May-2000
 C.Accession: T18511
 C.Description: R.Huang, J.; Oellies, J.; Johansen, K.M.; Johansen, J.
 A.Title: Characterization of the cDNA for the protein of Tractin and LeechCoM, two novel Ig-superfamily members
 A.Reference number: 218951; MUID:9746207; PMID:924388
 A.Accession: T18511
 A.Molecule type: mRNA
 A.Date: 1998-01-01
 A.Creation services: translated from GB/EWML/DD83
 A.Residues: 1-1880 <HUA>
 A.CCross-references: EMBL:U03813; NID:g275259; PID:g275260; PID:ACJ4754.1

Query Match
 Best Local Similarity 20.6%; Score 131.5; DB 2; Length 1880;
 Matches 87; Conservative 60; Mismatches 144; Indels 143; Gaps 19;

Qy 1 MDQCMGLSNHIFWATLGGAGKQLQAYFN-----ETADLQCF 42
 Db 1 WNYQ--APPLDGLATLLATNTQVWRPSTAMPPISTFKNWEVIFEA 97
 Qy 43 ANQNGSLSELVFN-QQENGLVNEVYVLEKFKFSVSKYKWTSGPDSNLTALNLQ 101

Db 58 TGT-----PLVCFMPTGCEPLESEA-----ERPFDQVQDTITLYNNE 97
 Qy 102 IDKGLQCIHQKPTG-----NIRHQMSSELSVLANFSGEIVPENTENYINLT 156
 Db 98 LLDSEYVQCIWNGKGTAAVWTLKAWQESFTV-----KEPQV--NVRGDNLLIA 150
 Qy 157 GSSHTGPEP-----KMSVLATPNS--TIEDQ-----IMNSQNVLTQVLS 200
 Db 151 CPPKSTPTDVYQTVKAGKLLPLNTNMYLDSNFFANWVE--EHRGQATLTC 208
 Qy 201 TGLSNG-PPYSNMTICTLSTFETWELLASPFLELDQPF-----241
 Db 209 ISHNWMSVQNDICILNNGSGQVGRGAWMTSPKDLATQSKKACIFSGY 268
 Qy 242 PPHLP-----ITAVP-----TVICWMP 263
 Db 269 PTPNVSIRGSDPPKIVNSSELPHELEIRNVDQAGTCTGSGTGAFFVDELT 328
 Qy 264 CILLNKKKKKRPN-----SYCKNTNMRSESE-QTAKSEKHPE--RSDR 309
 Db 329 VESPKKQNPEDQVTSDEBETAFVCGVGIPPTVWMLNMRLELPPRPMQND 388
 Qy 310 AGVFESKSTSCD 333
 Db 389 BERTVLSNVSBD 402

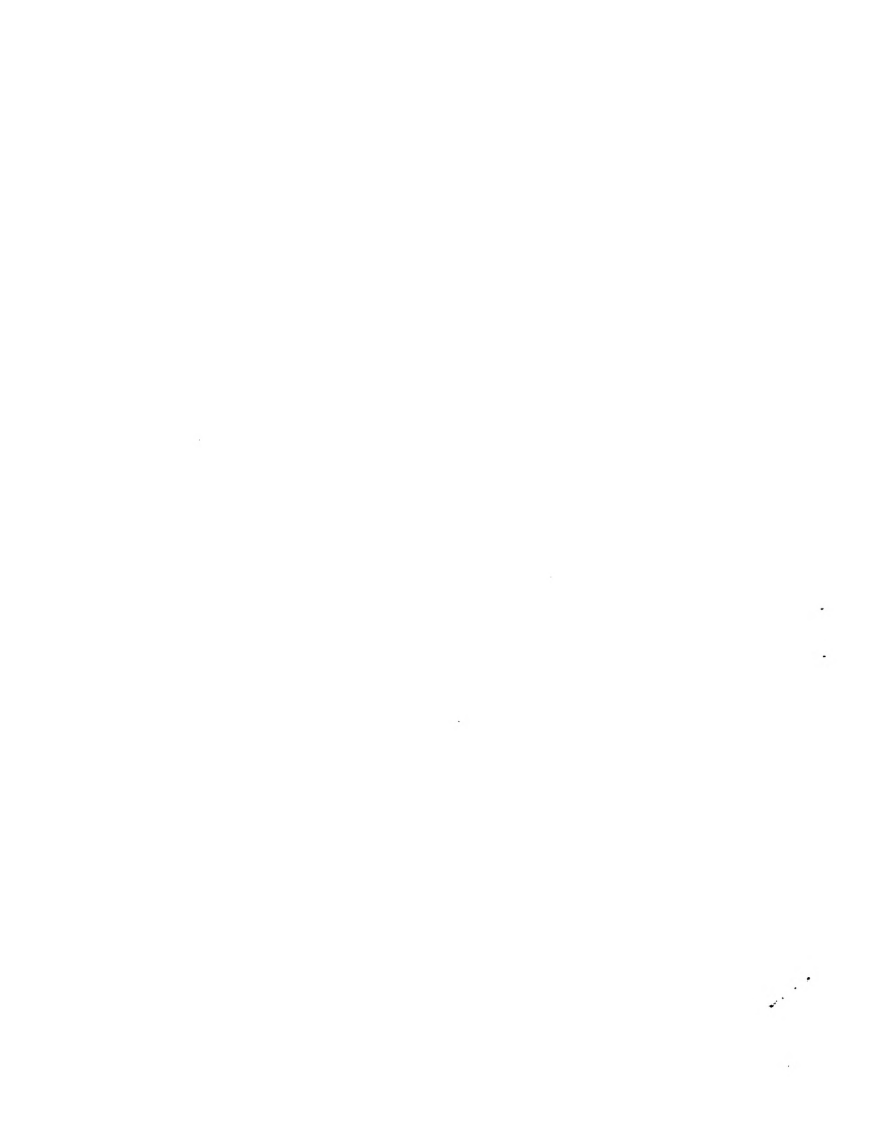
Search completed: February 13, 2003, 11:33:20
 Job time: 17.4702 secs

[illegible][illegible]

[illegible]

CC TESTED. IT IS EXPRESSED AT VERY LOW LEVELS ON ACTIVATED B CELLS
 CC -1. DEVELOPMENTAL STAGE: EXPRESSED AT LOW LEVELS ON PERIPHERAL T CELLS
 CC AND IS STONGLY UP-REGULATED AFTER ACTIVATION, PEAKING 6 TO 9 DAYS
 CC AFTER ACTIVATION.
 CC -1. SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC -1. SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE V-TYPE DOMAINS.
 CC -1. SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C-TYPE DOMAINS.
 CC -1. DATABASE: NMDB-PROT; NCBI CD 346; CD36
 CC WWW=ftp://www.ncbi.nlm.nih.gov/ncbi/cd36.htm.
 CC This Swiss-Prot entry is derived from the cDNA sequence
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use. The entry is derived from the cDNA sequence and has been modified
 CC modified and this statement is not removed upon "b" and for commercial
 CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
 CC or send an email to license@sib-sib.ch).
 CC
 CC EMBL: M8282; AAA3662.1; ..
 CC DR FR: A46472; A46462; ..
 CC DR FR: A46472; A46462; ..
 CC DR Plan: P00047; Ig; ..
 CC DR InterPro: IPR003006; Ig_MHC.
 CC DR
 CC KW Immunoglobulin domain; Glycoprotein; Transmembrane; Repeat; Signal.
 CC
 CC FT SIGNAL 1 21 POTENTIAL.
 CC FT CHAIN 22 569 T-CELL SURFACE PROTEIN TACTILE.
 CC FT TRANSHEM 502 525 POTENTIAL.
 CC FT DOMAIN 526 569 CYTOPLASMIC (POTENTIAL).
 CC FT DOMAIN 538 569 PRO-ITR-RICH.
 CC FT DOMAIN 538 569 PRO-ITR-RICH.
 CC FT DOMAIN 38 125 IG-LIKE V-TYPE DOMAIN 1.
 CC FT DOMAIN 156 238 IG-LIKE V-TYPE DOMAIN 2.
 CC FT DOMAIN 156 238 IG-LIKE V-TYPE DOMAIN.
 CC FT DISULFID 45 118 PROBABLE.
 CC FT DISULFID 163 231 PROBABLE.
 CC FT DISULFID 42 52 PROBABLE.
 CC FT CARBONHO 97 97 N-LINKED (GLNAC.) (POTENTIAL).
 CC FT CARBONHO 107 107 N-LINKED (GLNAC.) (POTENTIAL).
 CC FT CARBONHO 156 156 N-LINKED (GLNAC.) (POTENTIAL).
 CC FT CARBONHO 166 166 N-LINKED (GLNAC.) (POTENTIAL).
 CC FT CARBONHO 166 166 N-LINKED (GLNAC.) (POTENTIAL).
 CC FT CARBONHO 199 199 N-LINKED (GLNAC.) (POTENTIAL).
 CC FT CARBONHO 261 261 N-LINKED (GLNAC.) (POTENTIAL).
 CC FT CARBONHO 261 261 N-LINKED (GLNAC.) (POTENTIAL).
 CC FT CARBONHO 282 282 N-LINKED (GLNAC.) (POTENTIAL).
 CC FT CARBONHO 334 334 N-LINKED (GLNAC.) (POTENTIAL).
 CC FT CARBONHO 352 352 N-LINKED (GLNAC.) (POTENTIAL).
 CC FT CARBONHO 481 481 N-LINKED (GLNAC.) (POTENTIAL).
 CC FT CARBONHO 569 569 N-LINKED (GLNAC.) (POTENTIAL).
 CC
 CC Query Match 7.24; Score 124; DB 1; Length 569;
 CC Best Local Similarity 25.31; Pred. No. 0.037;
 CC Matches 63; Conservative 44; Mismatches 96; Indels 46; Gaps 15;
 CC
 CC QY 28 IOAYNTADLPQFANQNGSELVFPQGNVLEVTLAGKEFVSVMKGRIS 87
 CC DB 131 IETETNLEIPC-FOUSSSKISEFTYASVEIN-OTQETLLSQMLISNLTLLQRYK 208
 CC QY 88 FEGSDMTLRLHQLKNG-LVQCIIHKFKPTGIRHOMSELSVANFSQPEI-VPIS 145
 CC DB 209 LGTD-VLALSLYFQIDDKESQIR-VEGNKCLASITRYV-PAPKEPPIYE 260
 CC QY 146 NTEMVLT-NITSSHYPPFAMGVLRKNTST-EYQDGM-OMQSDVTEU 196
 CC DB 261 NSTDVLVERFTLLANVP-KANITWFDGSLHEDGIVTNEBKQDFEL 317
 CC QY 197 YNYSISLSGFFVMTSIFCI-LEDTK-TLEES-----PST-- 234

DB 318 KSVLTVSNKFAQSNLTHCALSPVQNVKWHVMSKIFLGLCEISLSTDPPLSYTE 377
 QY 235 ELSDQPPPP 243
 DB 378 STLTQDSEP 386
 Search completed: February 13, 2003, 11:31:39
 Job time : 19:5329 Recs



XX 28-OCT-1999. 99W0-1504674.
 XX 30-MAR-1999. 99W0-1504674.
 XX 17-APR-1998. 98U8-082220.
 XX 24-SEP-1998. 98U8-010580.
 XX 24-SEP-1998. 98U8-010580.
 XX (UYE-) UNIV VERMONT.
 XX Newell ME;
 XX WPI: 2000-08677/08.
 XX N-PSDB: A025921.
 XX Use of cell surface and membrane characteristics for developing
 XX products for treating cancers, autoimmune diseases or neurodegenerative
 XX diseases -
 XX Disclosure: Page 116-117; 123pp; English.
 XX The present sequence is human B7-2 co-stimulatory molecule. This is
 XX involved in stimulation of an immune response by its ability to interact
 XX with various immune cell surface receptors. The regulation of cell
 XX surface expression of MHC class II and co-stimulatory molecule B7 can be
 XX force which can be assessed in terms of mitochondrial membrane potential.
 XX These methods can be used for regulating cell growth and division to
 XX the expression of cell surface immune proteins. They can be used for
 XX treating diseases associated with excessive cellular division, aberrant
 XX differentiation, and premature cellular death, e.g. cancers, autoimmune
 XX diseases, neurodegenerative disorders etc.
 XX Sequence 323 AA;
 XX Query Match 97.9%; Score 1696; DB 21; Length 323;
 XX Best Local Similarity 100.0%; Pred. No. 2e-147;
 XX Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX 7 MELANLFWALLSGAARFKIAQVNETADLPQANQSLSLWVQDQBLN 66
 XX 1 MGSNLFPHWLLSGAARFKIAQVNETADLPQANQSLSLWVQDQBLN 60
 XX 67 EYLGLKSTFVHVKMGTFSDSMTLRJLNQKNGLYCIIHKKKPTMIRH 126
 XX 61 EYLGLKSTFVHVKMGTFSDSMTLRJLNQKNGLYCIIHKKKPTMIRH 120
 XX 127 NSESLVIANFSQPEVLSINTEVNIINTCSSIHOTPEPKNSVLRTNSTETD 186
 XX 121 NSESLVIANFSQPEVLSINTEVNIINTCSSIHOTPEPKNSVLRTNSTETD 180
 XX 187 QKSNQVNTLVYLSLSVPSDVTNTFICLETDKTLSSPSFTELEDPQPPH 246
 XX 181 QKSNQVNTLVYLSLSVPSDVTNTFICLETDKTLSSPSFTELEDPQPPH 240
 XX 247 PMTAVLPVLCVWVPLCLIMKKKKSPNSKCTGNTNMBEESCTKSEKHIP 306
 XX 241 PMTAVLPVLCVWVPLCLIMKKKKSPNSKCTGNTNMBEESCTKSEKHIP 300
 XX 307 SDEARVFNKSTSSCKSDCTCF 329
 XX 301 SDEARVFNKSTSSCKSDCTCF 323
 XX REUSE 8
 XX ID A025920 standard; Protein; 323 AA.
 XX A025920
 XX A025920
 XX A025920

DT 26-MAR-2002 (first entry)
 XX Human co-stimulatory molecule, B7-2 protein.
 XX Human: vaccine; immunostimulatory molecule; interferon; IFN; therapy;
 XX antigen presentation; vaccine; tumorigenesis; cancer; cytotoxic;
 XX antitumor; antibacterial; virucide; fungicide; protozoicide; B7-2.
 XX Homo sapiens.
 XX WQ200186097-A1.
 XX 22-NOV-2001.
 XX 17-MAY-2001; 2001NO-A000565.
 XX 17-MAY-2000; 2000AU-0007553.
 XX (NONG) UNIV MONASH.
 XX Ralph SJ;
 XX WPI: 2002-082990/11.
 XX N-PSDB: A025510.
 XX New composition, useful for treatment and/or prophylaxis of cancer and
 XX tumor, comprises immunostimulatory molecule and animal cells cultured
 XX in presence of interferon to enhance antigen presenting function of the
 XX cells.
 XX Claim 8; Page 102-103; 127pp; English.
 XX The present invention relates to a composition of matter comprising an
 XX immunostimulatory molecule and animal cells cultured in the presence of
 XX interferon to enhance antigen presenting function of the cells. The invention
 XX is used as vaccine. The composition is useful for treatment and/or
 XX prophylaxis of cancer and tumor, comprises immunostimulatory molecule and
 XX animal cells cultured in presence of interferon to enhance antigen presenting
 XX function of the cells. The composition, which comprises the soluble
 XX immunostimulatory molecule and the cultured animal cells is administered
 XX separately, sequentially or simultaneously to the patient. The present
 XX sequence is human co-stimulatory molecule, B7-2 protein.
 XX Sequence 323 AA;
 XX Query Match 97.9%; Score 1696; DB 23; Length 323;
 XX Best Local Similarity 100.0%; Pred. No. 2e-147;
 XX Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX 7 MELANLFWALLSGAARFKIAQVNETADLPQANQSLSLWVQDQBLN 66
 XX 1 MGSNLFPHWLLSGAARFKIAQVNETADLPQANQSLSLWVQDQBLN 60
 XX 67 EYLGLKSTFVHVKMGTFSDSMTLRJLNQKNGLYCIIHKKKPTMIRH 126
 XX 61 EYLGLKSTFVHVKMGTFSDSMTLRJLNQKNGLYCIIHKKKPTMIRH 120
 XX 127 NSESLVIANFSQPEVLSINTEVNIINTCSSIHOTPEPKNSVLRTNSTETD 186
 XX 121 NSESLVIANFSQPEVLSINTEVNIINTCSSIHOTPEPKNSVLRTNSTETD 180
 XX 187 QKSNQVNTLVYLSLSVPSDVTNTFICLETDKTLSSPSFTELEDPQPPH 246
 XX 181 QKSNQVNTLVYLSLSVPSDVTNTFICLETDKTLSSPSFTELEDPQPPH 240
 XX 247 PMTAVLPVLCVWVPLCLIMKKKKSPNSKCTGNTNMBEESCTKSEKHIP 306
 XX 241 PMTAVLPVLCVWVPLCLIMKKKKSPNSKCTGNTNMBEESCTKSEKHIP 300
 XX 307 SDEARVFNKSTSSCKSDCTCF 329
 XX 301 SDEARVFNKSTSSCKSDCTCF 323

CC acide 5-106 from porcine CM6. It is encoded by a DNA construct
 CC (AA62939) obtd. by PCR amplification of porcine sequences and
 CC ligation to a sequence encoding the C-terminal region of human
 CC CD80 protein. The region of the CD80 protein that was used for
 CC subcloning was from amino acid 191 to 245. The CD80 protein
 CC was expressed in HEK293 cells. Antisera to porcine
 CC CD80 protein, P-selectin (see also AA01945) and vascular cell
 CC adhesion molecule (see also AA01931-42) are useful for diagnosing
 CC endothelial dysfunction and for studying the role of these
 CC molecules in the pathogenesis of atherosclerosis and in
 CC xenotransplantation of porcine cells, tissues and organs into human
 CC recipients.

50 Sequence 250 AA;
 Query Match 57/24; Score 99; DB 18; Length 250;
 Ids Similarity 76.0%; Positives 19; Mismatches 0; Gaps 0;
 Match 191; Conservative 19; Indels 0;
 QY 1 MDPCCTGCLNLTFFNAYLLGGALPILKTONYFETADLPCCFANSGNGLSELVTFNQDQ 60
 DB 1 MDPCCTGCLNLTFFNAYLLGGALPILKTONYFETADLPCCFANSGNGLSELVTFNQDQ 60
 QY 61 ENLVNLYVKNKEDSVNSKYWRTSDPSNTLJAHNQLKNGLYOCIIHKKPTOM 120
 DB 61 ENLVNLYVKNKEDSVNSKYWRTSDPSNTLJAHNQLKNGLYOCIIHKKPTOM 120
 QY 61 DNLVLYETGCKEPHNSKYWRTSDPSNTLJAHNQLKNGLYOCIIHKKPTOM 120
 DB 61 DNLVLYETGCKEPHNSKYWRTSDPSNTLJAHNQLKNGLYOCIIHKKPTOM 120
 QY 121 IRIHOMSELVANFQPEIVFSINTEVINTCSIHGYPEKDNQSVLLRTASTI 180
 DB 121 IRIHOMSELVANFQPEIVFSINTEVINTCSIHGYPEKDNQSVLLRTASTI 180
 QY 181 EYDGIKNSQNVLYETVNSISLVSPDVSMTIFCIETKTLSSPPSLSDPQ 240
 DB 181 EYDGIKNSQNVLYETVNSISLVSPDVSMTIFCIETKTLSSPPSLSDPQ 240
 QY 241 PPPDH 245
 DB 241 PPPDH 245

Search Completed: February 13, 2003, 11:30:58
 Job time : 37:55:02 secs


```

APPLICATION NUMBER: US 07/864,866
FILING DATE: 7-APR-1992
PUBLICATION NUMBER: US 08/218,155
PUBLICATION DATE: 12-APR-1992
APPLICATION NUMBER: US 07/864,807
FILING DATE: 7-APR-1992
PUBLICATION NUMBER: US 08/218,155
PUBLICATION DATE: 12-APR-1992
APPLICATION NUMBER: US 07/275,433
FILING DATE: 23-NOV-1988
PUBLICATION NUMBER: 1-APR-1992
ATTORNEY: Mandagoules, Amy E.
REGISTRATION NUMBER: 34,207
REGISTRATION DATE: 1-APR-1992
TELEPHONE: (617) 227-7400
TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 227-5941
INVENTOR: Mandagoules, Amy E.
SEQUENCE CHARACTERISTICS: 4:
LENGTH: 325 amino acids
TOPOLOGICAL:
MOLECULE TYPE: protein
US-08-592-711-4

Query Match
Best Local Similarity 100.0%; Score 1733; DB 8; Length 329;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MDPOCTGLNLSLFWNAFLGAPLQATYFNATDLQCFANSSQSLSELVFMQD 60
DB 1 MDPOCTGLNLSLFWNAFLGAPLQATYFNATDLQCFANSSQSLSELVFMQD 60
Oy 61 ENLVNVEYLGKRFVSKWMTSPFSDGNTLRJLNQIKKGLQCTIHHKPTGN 120
DB 61 ENLVNVEYLGKRFVSKWMTSPFSDGNTLRJLNQIKKGLQCTIHHKPTGN 120
Oy 121 IRHOMSELSYLANFSPVPIENTVNTVLTCSIHGYEPKMSVLATNSTI 180
DB 121 IRHOMSELSYLANFSPVPIENTVNTVLTCSIHGYEPKMSVLATNSTI 180
Oy 131 RHOMSELSYLANFSPVPIENTVNTVLTCSIHGYEPKMSVLATNSTI 180
DB 131 RHOMSELSYLANFSPVPIENTVNTVLTCSIHGYEPKMSVLATNSTI 180
Oy 181 EYGIWMSQDNVTELYDGLSLSGSPDVSNMTICLETDTKTLSSPFILEDQ 240
DB 181 EYGIWMSQDNVTELYDGLSLSGSPDVSNMTICLETDTKTLSSPFILEDQ 240
Oy 241 PPDIHPMTAVLPVTCWVFCFLMKKKKRPKNYKCTNMTRESSEOTKKRK 300
DB 241 PPDIHPMTAVLPVTCWVFCFLMKKKKRPKNYKCTNMTRESSEOTKKRK 300
Oy 301 IHPRSDGQVFKSKTSCKSDSTCF 329
DB 301 IHPRSDGQVFKSKTSCKSDSTCF 329

RESULT 3
US-09-837-867A-23
; Sequence 23, Application US/09837867A
; BEST LOCAL SIMILARITY 100.0%; SCORE 1733; DB 10; LENGTH 329;
; MATCHES 329; CONSERVATIVE 0; MISMATCHES 0; INDELS 0; GAPS 0;
; ORGANISM: Homo sapiens
; GENERAL INFORMATION
; APPLICANT: Sharp, Ariene H.
; APPLICANT: Borriello, Franco E.
; APPLICANT: Nadler, Lee M.
; TITLE OF INVENTION: NO. US020098542461: FORMS OF T CELL COSTIMULATORY
; FILE REFERENCE: SM-120FADV
; CURRENT APPLICATION NUMBER: US/09/837,867A
; PRIOR FILING DATE: 1994-03-02
; NUMBER OF SEQ ID NOS: 42
; SEQ ID NO 23
; SEQ ID NO 23
; LENGTH: 329
; TYPE: PROT
; ORGANISM: Homo sapiens
US-09-837-867A-23

Query Match
Best Local Similarity 100.0%; Score 1713; DB 10; Length 329;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MDPOCTGLNLSLFWNAFLGAPLQATYFNATDLQCFANSSQSLSELVFMQD 60
DB 1 MDPOCTGLNLSLFWNAFLGAPLQATYFNATDLQCFANSSQSLSELVFMQD 60
Oy 61 ENLVNVEYLGKRFVSKWMTSPFSDGNTLRJLNQIKKGLQCTIHHKPTGN 120
DB 61 ENLVNVEYLGKRFVSKWMTSPFSDGNTLRJLNQIKKGLQCTIHHKPTGN 120
Oy 121 IRHOMSELSYLANFSPVPIENTVNTVLTCSIHGYEPKMSVLATNSTI 180
DB 121 IRHOMSELSYLANFSPVPIENTVNTVLTCSIHGYEPKMSVLATNSTI 180
Oy 181 EYGIWMSQDNVTELYDGLSLSGSPDVSNMTICLETDTKTLSSPFILEDQ 240
DB 181 EYGIWMSQDNVTELYDGLSLSGSPDVSNMTICLETDTKTLSSPFILEDQ 240

SEQUENCE 2
US-09-441-411-26
; Sequence 26, Application US/0944111
; Publication No. US20030008342A1
; BEST LOCAL SIMILARITY 100.0%; SCORE 1723; DB 9; LENGTH 329;
; MATCHES 329; CONSERVATIVE 0; MISMATCHES 0; INDELS 0; GAPS 0;
; ORGANISM: Homo sapiens
; GENERAL INFORMATION
; APPLICANT: Scholler, Nathalie B.
; APPLICANT: Diels, Mary L.
; APPLICANT: Hellercom, Ingeborg
; APPLICANT: Hellercom, Rick
; TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
; FILE REFERENCE: 730033,409 US/09/441,411
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 1
; SEQ ID NO 26
; SEQ ID NO 26
; LENGTH: 329
; TYPE: PROT
; ORGANISM: Homo sapiens

```



```

Query Match      42.94, Score 743.5; DB 9; Length 309;
Rec. Local Similarity 51.54; Pred. No. 5e-49;
Matches 198; Consensitive 45; Mismatches 51; Indels 13; Gaps 5;

Qy 1 MDPCINLSNIFWAFLLGAPFLXIONFETALPQOPANQSLSELVFNQO 60
Db 1 MDPCINLSNIFWAFLLGAPFLXIONFETALPQOPANQSLSELVFNQO 60
Qy 61 ENKLVNRYLGRKRTSDHEKYMRTSPDSMTLRLNQLIKDGLYOCIIHKKKPTOM 120
Db 61 ENKLVNRYLGRKRTSDHEKYMRTSPDSMTLRLNQLIKDGLYOCIIHKKKPTOM 120
Qy 121 TELVQNSRELVLNAGSOPVWPIWNTENTVNLTCGSHVEYFKNQSVLFTKNTI 180
Db 121 TELVQNSRELVLNAGSOPVWPIWNTENTVNLTCGSHVEYFKNQSVLFTKNTI 180
Qy 181 EYDGMKQSDNYTELYDVISLSVSPDVTGNTIFCLLTDKTELSSPFSLEDPQ 240
Db 181 EYDGMKQSDNYTELYDVISLSVSPDVTGNTIFCLLTDKTELSSPFSLEDPQ 240
Qy 179 EYDGMQISQDNYTELYDVISLSVSPDVTGNTIFCLLTDKTELSSPFSLEDPQ 238
Db 179 EYDGMQISQDNYTELYDVISLSVSPDVTGNTIFCLLTDKTELSSPFSLEDPQ 238
Qy 241 PPDHPH4--ITAVLPTVICWVCLLWKKKKKPFNSTYCGTNTVREESOTKAR 298
Db 239 P--OTTAKETITATVALLWL--LIVCKSQPQSRP---SNTAKLQSDNAOR 289
Qy 289 EKIHPE 305
Db 280 ETLNKE 296

```

Search completed, February 13, 2003, 11:39:57
 Job time : 13.0466 sec

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 13, 2003, 11:29:49, Search time 12.8918 seconds
(without alignments)

Title: US-09-425-516-2
750,873 Million cell updates/sec

Perfect score: 1
Sequence: 1 MDPCTWGLNLIPLWML.....ADRVKSTSCSKSTJCF 129

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

1: /csm2_6/prodatat/1/ia/58 COMB.ppp:

2: /csm2_6/prodatat/1/ia/58 COMB.ppp:

3: /csm2_6/prodatat/1/ia/58 COMB.ppp:

4: /csm2_6/prodatat/1/ia/58 COMB.ppp:

5: /csm2_6/prodatat/1/ia/58 COMB.ppp:

6: /csm2_6/prodatat/1/ia/backfile1.ppp:

Prod. No. is the number of results predicted by chance to have a

score greater than the observed score being printed.

and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Length	DB	ID	Description
1	1713	100.0	329	2	US-08-456-104-2	Sequence 2, Appl	
2	1713	100.0	329	2	US-08-101-544-2	Sequence 2, Appl	
3	1713	100.0	329	2	US-08-280-7578-2	Sequence 2, Appl	
4	1713	100.0	329	4	US-08-205-6974-23	Sequence 23, Appl	
5	1713	100.0	329	4	US-08-205-6974-23	Sequence 23, Appl	
6	1713	100.0	329	4	US-08-205-6974-23	Sequence 23, Appl	
7	1713	100.0	329	4	US-08-205-6974-23	Sequence 23, Appl	
8	1713	100.0	329	5	PCT-US95-02574-23	Sequence 23, Appl	
9	1713	100.0	329	5	PCT-US95-02574-23	Sequence 23, Appl	
10	1696	97.9	325	5	PCT-US94-09842-2	Sequence 2, Appl	
11	1696	97.9	325	5	PCT-US94-09842-2	Sequence 2, Appl	
12	953	95.0	325	4	US-09-451-200-20	Sequence 18, Appl	
13	953	95.0	325	4	US-09-451-200-19	Sequence 18, Appl	
14	743.5	42.9	309	2	US-08-456-104-2	Sequence 4, Appl	
15	743.5	42.9	309	3	US-08-478-7448-23	Sequence 23, Appl	
16	743.5	42.9	309	3	US-08-478-7448-23	Sequence 23, Appl	
17	743.5	42.9	309	4	US-08-205-6974-23	Sequence 23, Appl	
18	743.5	42.9	309	4	US-08-205-6974-23	Sequence 23, Appl	
19	743.5	42.9	309	5	US-08-451-200-20	Sequence 22, Appl	
20	743.5	42.9	309	5	PCT-US95-02574-23	Sequence 21, Appl	
21	724.5	41.8	314	4	US-08-205-6974-13	Sequence 13, Appl	
22	724.5	41.8	314	4	US-08-205-6974-13	Sequence 13, Appl	
23	724.5	41.8	314	4	PCT-US95-02574-23	Sequence 13, Appl	
24	710.5	41.0	303	4	US-09-451-200-23	Sequence 23, Appl	
25	597	33.3	110	3	US-08-478-7448-45	Sequence 45, Appl	
26	597	33.3	110	3	US-08-478-7448-45	Sequence 45, Appl	
27	517	23.8	102	3	US-08-280-7578-47	Sequence 47, Appl	

28	517	29.8	102	4	US-08-280-7578-47	Sequence 47, Appl
29	328	18.9	61	4	US-08-205-6974-32	Sequence 32, Appl
30	328	18.9	61	4	US-08-702-424-32	Sequence 32, Appl
31	328	18.9	61	4	US-08-702-424-32	Sequence 32, Appl
32	328	18.9	95	4	US-08-938-180B-10	Sequence 10, Appl
33	245.5	14.2	320	4	US-08-205-6974-2	Sequence 2, Appl
34	245.5	14.2	320	4	US-08-205-6974-2	Sequence 2, Appl
35	245.5	14.2	320	4	US-08-205-6974-2	Sequence 2, Appl
36	244	14.1	306	4	US-08-205-6974-17	Sequence 17, Appl
37	244	14.1	306	4	US-08-702-525-17	Sequence 17, Appl
38	244	14.1	306	4	US-08-702-525-17	Sequence 17, Appl
39	244	14.1	306	5	PCT-US95-0576-17	Sequence 17, Appl
40	243	14.0	299	4	US-09-651-200-15	Sequence 15, Appl
41	243	14.0	299	4	US-09-651-200-15	Sequence 15, Appl
42	242	14.0	306	2	US-08-456-104-8	Sequence 8, Appl
43	242	14.0	306	2	US-08-101-624-25	Sequence 25, Appl
44	242	14.0	306	3	US-08-153-462-25	Sequence 25, Appl
45	242	14.0	306	3	US-08-475-7448-31	Sequence 31, Appl

ALIGNMENTS

RESULT 1

Sequence 2, Application US/08456104

Patent No. 586310

Applicant: Freeman, Gordon J.

Applicant: Nadler, Lee M.

Title of Invention: Tumor Cells Modified to Express B7-2 and B7-3 With Increased

Number of Sequences: 8

Correspondence Address: COCKFIELD

ATTORNEYS AT LAW, 100 STATE STREET, 6TH FLOOR, SUITE 510

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM: disk

OPERATING SYSTEM: PC-DOS/MS-DOS

COMPUTER: IBM PC compatible

Version #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/456.104

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/101,624,

APPLICATION NUMBER: 08/109,393;

APPLICATION NUMBER: 19-AUG-1993;

NAME: Mandrasco, Jay E.

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: RPI-008

TELEPHONE: (617) 227-7400

TELEFAX: (617) 227-5941

IMPORTANCE: 2

SEQUENCE CHARACTERISTICS:

LENGTH: 329 amino acids

TOPOLOG: amino acid

MOLECULE TYPE: protein

US-08-456-104-2

Query Match 100.0%, Score 1733, DB 2, Length 329,
Best Local Similarity 100.0%, Pred. No. 4, Je-154,
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

```

Oy 1 MPOCTMGLSILFWAFLLGGAFLKQAYNETADLPCOFANSQNSLSLWPMQD 60
Db 1 MPOCTMGLSILFWAFLLGGAFLKQAYNETADLPCOFANSQNSLSLWPMQD 60
Oy 61 ENLUNLVETGKEFESUNYNGKTSFDSBWTBLRHLQIKOKGLYQCIHUKKPTON 120
Db 61 ENLUNLVETGKEFESUNYNGKTSFDSBWTBLRHLQIKOKGLYQCIHUKKPTON 120
Oy 63 ENLUNLVETGKEFESUNYNGKTSFDSBWTBLRHLQIKOKGLYQCIHUKKPTON 120
Db 63 ENLUNLVETGKEFESUNYNGKTSFDSBWTBLRHLQIKOKGLYQCIHUKKPTON 120
Oy 121 ITHOMSELVSLANFQSPREPIVNTENYNTICSHGYTPFKMGSVLATNNTI 180
Db 121 ITHOMSELVSLANFQSPREPIVNTENYNTICSHGYTPFKMGSVLATNNTI 180
Oy 181 ETCIMQSKQNTVELYDNLISLVSFVPSVNTIFCILETNTKLLSPFSLERPD 240
Db 181 ETCIMQSKQNTVELYDNLISLVSFVPSVNTIFCILETNTKLLSPFSLERPD 240
Oy 241 EPRHEPNTLWPTVLCVWFFCLLWKKKKKPRNSKQNTNMRERESOTKREK 300
Db 241 EPRHEPNTLWPTVLCVWFFCLLWKKKKKPRNSKQNTNMRERESOTKREK 300
Oy 243 PPRHPIWTAUPLVFCVWFFCLLWKKKKKPRNSKQNTNMRERESOTKREK 300
Db 243 PPRHPIWTAUPLVFCVWFFCLLWKKKKKPRNSKQNTNMRERESOTKREK 300
Oy 301 IHIFRSDEARVFSKTSCKSDCTCF 329
Db 301 IHIFRSDEARVFSKTSCKSDCTCF 329
Oy 303 IHIFRSDEARVFSKTSCKSDCTCF 329
Db 303 IHIFRSDEARVFSKTSCKSDCTCF 329

RESULT 2 624-2
Sequence 2, Application US/08101624
GENERAL INFORMATION:
PATENT NO. 5442607
APPLICANT: RADLEY, Lee M.
INVENTOR: RADLEY, Lee M.
TITLE OF INVENTION: Bases Therefor
NUMBER OF SEQUENCES: 25
COMPARISON ADDRESS: COCKFIELD
COMPARISON ADDRESS: LAUREL & COCKFIELD, LLP
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPARISON ADDRESS: KPMG
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE SYSTEM: PC DOS/MS DOS
SOFTWARE PATENT IN: Patent In Base #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08101,624
APPLICATION NUMBER: US/08101,624
FILING DATE: 28-JULY-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
PUBLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mandregoures, Amy E.
REFERENCE/DOCKET NUMBER: SPT-004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-5541
TELEFAX: (617) 227-5541
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
TYPE: amino acid
TOPOLOGY: linear
MOLECULAR TYPE: protein
US-08-101,624-2
Query Match
Best Local Similarity 100.0% Score 1733 Db 2 Length 329
Matches 329 Conservative 0 Mismatches 0 Indels 0 Gaps 0

```

```

; TOPLOGY: linear
; MOLECULE TYPE: protein
US-08-478-741A-2
Query Watch
Best Local Similarity 100.0%; Score 1733; DB 3; Length 329;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPOCTMGLSNTLPAFLLSGAPAKIQVNFETADLPCOFANSONSLSLVFMDQ 60
Db 1 MPOCTMGLSNTLPAFLLSGAPAKIQVNFETADLPCOFANSONSLSLVFMDQ 60
Qy 61 ENLNUVMEYLVKAEFVSQWYKTSFDSQSMTLRLNLIQKNGVQCIHHKPTGM 120
Db 61 ENLNUVMEYLVKAEFVSQWYKTSFDSQSMTLRLNLIQKNGVQCIHHKPTGM 120
Qy 121 RIHQNSSELVLANSPREIVSNITENYINLTCSIHOTPEKNSVLATNSTI 180
Db 121 RIHQNSSELVLANSPREIVSNITENYINLTCSIHOTPEKNSVLATNSTI 180
Qy 181 EYQMKQSNQNTLYDVISLSLVFVPSVNTIFCLTETKTLISLSPFSELDQ 240
Db 181 EYQMKQSNQNTLYDVISLSLVFVPSVNTIFCLTETKTLISLSPFSELDQ 240
Qy 241 PPDHHPMTAVLPVTCVWVFCFLLMWKKKKPRPNKYCGTNNHRESBOTKREK 300
Db 241 PPDHHPMTAVLPVTCVWVFCFLLMWKKKKPRPNKYCGTNNHRESBOTKREK 300
Qy 301 IHPIESDAQVFKSKTSCKDSQTCF 329
Db 301 IHPIESDAQVFKSKTSCKDSQTCF 329
; Sequence 2, Application US/082807578
; Patent No. 610316
; GRANT INFORMATION
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; APPLICANT: Gray, Gary
; APPLICANT: Ewald
; TITLE OF INVENTION: No. 61031661 CTLA4/CD28 Ligands and
; TITLE OF INVENTION: Use Thereof
; CORRESPONDENCE ADDRESS
; ADDRESSEE: LAHIVE & COCKFIELD
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: 08/08/08-7578
; FILING DATE: 26-JUL-1994
; CLASSIFICATION: 435
; PRIORITY DATA: 08/101.624
; APPLICATION NUMBER: 08/101.624
; FILING DATE: 26-JUL-1993
; PRIORITY NUMBER: 08/09.393
; APPLICATION NUMBER: 08/147.773
; FILING DATE: 3-NOV-1993
; NAME: Mandagouane, Any E
; REGISTRATION NUMBER: 36, 207
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO. 2:
; SOURCE: Characterized
; LENGTH: 329 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-280-757B-2
Query Watch
Best Local Similarity 100.0%; Score 1733; DB 4; Length 329;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPOCTMGLSNTLPAFLLSGAPAKIQVNFETADLPCOFANSONSLSLVFMDQ 60
Db 1 MPOCTMGLSNTLPAFLLSGAPAKIQVNFETADLPCOFANSONSLSLVFMDQ 60
Qy 61 ENLNUVMEYLVKAEFVSQWYKTSFDSQSMTLRLNLIQKNGVQCIHHKPTGM 120
Db 61 ENLNUVMEYLVKAEFVSQWYKTSFDSQSMTLRLNLIQKNGVQCIHHKPTGM 120
Qy 121 RIHQNSSELVLANSPREIVSNITENYINLTCSIHOTPEKNSVLATNSTI 180
Db 121 RIHQNSSELVLANSPREIVSNITENYINLTCSIHOTPEKNSVLATNSTI 180
Qy 181 EYQMKQSNQNTLYDVISLSLVFVPSVNTIFCLTETKTLISLSPFSELDQ 240
Db 181 EYQMKQSNQNTLYDVISLSLVFVPSVNTIFCLTETKTLISLSPFSELDQ 240
Qy 241 PPDHHPMTAVLPVTCVWVFCFLLMWKKKKPRPNKYCGTNNHRESBOTKREK 300
Db 241 PPDHHPMTAVLPVTCVWVFCFLLMWKKKKPRPNKYCGTNNHRESBOTKREK 300
Qy 301 IHPIESDAQVFKSKTSCKDSQTCF 329
Db 301 IHPIESDAQVFKSKTSCKDSQTCF 329
; Sequence 2, Application US/08205977A
; Patent No. 6218510
; GRANT INFORMATION
; APPLICANT: Actelion AG
; APPLICANT: Borriello, Francesco Paolo
; APPLICANT: Freeman, Gordon J.
; TITLE OF INVENTION: No. 6218510el Forms of T Cell Costimulatory Molecules
; TITLE OF INVENTION: Use Thereof
; CORRESPONDENCE ADDRESS
; ADDRESSEE: LAHIVE & COCKFIELD
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: SASII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/205,697A
; FILING DATE: 08/08/08-7578
; APPLICATION NUMBER: 08/147.773
; FILING DATE: 3-NOV-1993
; NAME: Mandagouane, Any E
; REGISTRATION NUMBER: 36, 207
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941

```

```

/ INFORMATION FOR SEQ ID NO: 23:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 329 amino acids
/ INITIATION: start codon is at position 1
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-05-697A-23

Query Match      100.0%   Score 1733;   DB 4;   Length 329;
Best Local Similarity 100.0%;   Ident. No. 4,3e-154;   Indels 0;   Gaps 0;
Patches 329;   Conservative 0;   Mismatches 0;

Db 1 MPOCTMGISLTFPMALFISGAAPKIQATFNETALDQCFANSQNSLSSELVFWQD 60
Oy 1 MPOCTMGISLTFPMALFISGAAPKIQATFNETALDQCFANSQNSLSSELVFWQD 60
Db 61 ENLUMVETLKQFETSHVSWKTSFSSSTLILANLQIKQKGLQCILHKKPTQM 120
Oy 61 ENLUMVETLKQFETSHVSWKTSFSSSTLILANLQIKQKGLQCILHKKPTQM 120
Db 61 ENLUMVETLKQFETSHVSWKTSFSSSTLILANLQIKQKGLQCILHKKPTQM 120
Oy 121 ITHOMSESLVLANFQSPVLSNTENVYINUTCSHIFEPKMSVLAFTNSTI 180
Db 121 ITHOMSESLVLANFQSPVLSNTENVYINUTCSHIFEPKMSVLAFTNSTI 180
Oy 121 ITHOMSESLVLANFQSPVLSNTENVYINUTCSHIFEPKMSVLAFTNSTI 180
Db 121 ITHOMSESLVLANFQSPVLSNTENVYINUTCSHIFEPKMSVLAFTNSTI 180
Oy 181 ETGCMQSQNDVLELYDVISLSVFPDVSMTIFCLTETKTLASLSPFELEDPQ 240
Db 181 ETGCMQSQNDVLELYDVISLSVFPDVSMTIFCLTETKTLASLSPFELEDPQ 240
Oy 181 ETGCMQSQNDVLELYDVISLSVFPDVSMTIFCLTETKTLASLSPFELEDPQ 240
Db 181 ETGCMQSQNDVLELYDVISLSVFPDVSMTIFCLTETKTLASLSPFELEDPQ 240
Oy 241 PPDHLPMTAVLPVILCWVFLILMMKKKKRPNSTKCTNTMREBSQTKREK 300
Db 241 PPDHLPMTAVLPVILCWVFLILMMKKKKRPNSTKCTNTMREBSQTKREK 300
Oy 241 PPDHLPMTAVLPVILCWVFLILMMKKKKRPNSTKCTNTMREBSQTKREK 300
Db 241 PPDHLPMTAVLPVILCWVFLILMMKKKKRPNSTKCTNTMREBSQTKREK 300
Oy 301 IHIPESDQARVFKSKTSCKSDSTCF 329
Db 301 IHIPESDQARVFKSKTSCKSDSTCF 329
Oy 301 IHIPESDQARVFKSKTSCKSDSTCF 329
Db 301 IHIPESDQARVFKSKTSCKSDSTCF 329

RESULT 7
/ Sequence 4, Application US/08403253A
/ Applicant: June, Carl H., Thompson, Craig H., Nabel, Gary J.
/ GENERAL INFORMATION:
/ APPLICANT: June, Carl H., Thompson, Craig H., Nabel, Gary J.
/ TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells
/ NUMBER OF SEQUENCES: 14
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE 28 LANIUS & COCKFIELD
/ STREET: 28 State Street
/ CITY: Boston
/ STATE: Massachusetts
/ COUNTRY: USA
/ ZIP: 02109
/ COMPUTER READABLE FORM:
/ COMPUTER TYPE: floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: ASCII Text
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/403,253A
/ PRIORITY INFORMATION:
/ PRIORITY DATE: 02 Mar 1994
/ PRIORITY NUMBER: US 08/253,964
/ FILING DATE: 4 JUNE 1993
/ FILING NUMBER: US 08/071,223
/ PENDING DATE: 23 FEB 1994
/ PENDING NUMBER: US 07/864,805
/ APPLICATION NUMBER: US 08/247,505

```


FILING DATE: 23 MAY 1994
 APPLICATION NUMBER: US 07/864,866
 PCT NO.: 93/02576
 APPLICATION NUMBER: US 08/218,155
 FILING DATE: 25 MAR 1994
 PCT NO.: 93/02576
 APPLICATION NUMBER: US 07/864,807
 FILING DATE: 25 MAR 1994
 APPLICATION NUMBER: US 07/902,457
 FILING DATE: 16 JUNE 1992
 APPLICATION NUMBER: US 07/775,433
 FILING DATE: 21 NOV 1988
 ATTORNEY/AGENT INFORMATION:
 NAME: ROBERT A. ROBERTS, JR.
 REGISTRATION NUMBER: 66 207
 REFERENCE/DOCKET NUMBER: RPI-003CF2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 742-4214
 TELEFAX: (617) 742-4214
 INFORMATION FOR SEQ ID NO: 4:
 TYPE: amino acid
 LENGTH: 329 amino acids
 TOPOLOGY: linear
 MOLECULAR WEIGHT: protein
 US-08-403-251A-4

Query Match 100.00, Score 1333, DB 5, Length 329,
 Best Local Similarity 100.00, Pct No. 4, 3e-154,
 Matches 329, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

Oy 1 MDPOCTMGLSNTLFWALFLSGAALUKIOAYNETADLPQFANSONGSELVYFMDQ 60
 Db 1 MDPOCTMGLSNTLFWALFLSGAALUKIOAYNETADLPQFANSONGSELVYFMDQ 60
 Oy 61 ENULNEVYLGRKESQSYKHYKWTFSFGSPTLRLNLQIKDGLVOCIHHKKPTOM 120
 Db 61 ENULNEVYLGRKESQSYKHYKWTFSFGSPTLRLNLQIKDGLVOCIHHKKPTOM 120
 Oy 121 IRHOMSELVLANFSOPELVINTEVNTICSSINOTPEKNSVLLRTNSTI 180
 Db 121 IRHOMSELVLANFSOPELVINTEVNTICSSINOTPEKNSVLLRTNSTI 180
 Oy 181 EYDIHQKQNTVELVDNISLSVGFDDVTSMTIFCLDTKLTLSGSPSILEDQ 240
 Db 181 EYDIHQKQNTVELVDNISLSVGFDDVTSMTIFCLDTKLTLSGSPSILEDQ 240
 Oy 241 PPDHPIWTAVLPTVLCVWVFLCLLMMKKCKPRNSKCGTTHREESQTKREK 300
 Db 241 PPDHPIWTAVLPTVLCVWVFLCLLMMKKCKPRNSKCGTTHREESQTKREK 300
 Oy 301 IHPERESQAQRFKSSKTSCKSDTCF 329
 Db 301 IHPERESQAQRFKSSKTSCKSDTCF 329

RESULT 8
 PCT-US95-02576-23
 GENERAL INFORMATION:
 APPLICANT: National Cancer Institute
 TITLE OF INVENTION: Novel Form of T cell Costimulatory Molecules
 NUMBER OF SEQUENCES: 65
 CORRESPONDENCE ADDRESS: COOKFIELD
 STREET: 60 State Street, suite 510
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02109-1875
 COMPUTER READABLE FORM: disk
 COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII Text
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT-US95/02576
 FILING DATE:
 PRIOR APPLICATION DATA: US 08/205,697
 FILING DATE: 02-MAR-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: ROBERT A. ROBERTS, JR.
 REGISTRATION NUMBER: 66 207
 REFERENCE/DOCKET NUMBER: BM-120CPFC
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 742-4214
 TELEFAX: (617) 742-4214
 INFORMATION FOR SEQ ID NO: 23:
 TYPE: amino acid
 LENGTH: 329 amino acids
 TOPOLOGY: linear
 MOLECULAR WEIGHT: protein
 PCT-US95-02576-23

Query Match 100.00, Score 1333, DB 5, Length 329,
 Best Local Similarity 100.00, Pct No. 4, 3e-154,
 Matches 329, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

Oy 1 MDPOCTMGLSNTLFWALFLSGAALUKIOAYNETADLPQFANSONGSELVYFMDQ 60
 Db 1 MDPOCTMGLSNTLFWALFLSGAALUKIOAYNETADLPQFANSONGSELVYFMDQ 60
 Oy 61 ENULNEVYLGRKESQSYKHYKWTFSFGSPTLRLNLQIKDGLVOCIHHKKPTOM 120
 Db 61 ENULNEVYLGRKESQSYKHYKWTFSFGSPTLRLNLQIKDGLVOCIHHKKPTOM 120
 Oy 121 IRHOMSELVLANFSOPELVINTEVNTICSSINOTPEKNSVLLRTNSTI 180
 Db 121 IRHOMSELVLANFSOPELVINTEVNTICSSINOTPEKNSVLLRTNSTI 180
 Oy 181 EYDIHQKQNTVELVDNISLSVGFDDVTSMTIFCLDTKLTLSGSPSILEDQ 240
 Db 181 EYDIHQKQNTVELVDNISLSVGFDDVTSMTIFCLDTKLTLSGSPSILEDQ 240
 Oy 241 PPDHPIWTAVLPTVLCVWVFLCLLMMKKCKPRNSKCGTTHREESQTKREK 300
 Db 241 PPDHPIWTAVLPTVLCVWVFLCLLMMKKCKPRNSKCGTTHREESQTKREK 300
 Oy 301 IHPERESQAQRFKSSKTSCKSDTCF 329
 Db 301 IHPERESQAQRFKSSKTSCKSDTCF 329

RESULT 9
 US-09-451-200-21
 GENERAL INFORMATION:
 APPLICANT: National Cancer Institute
 TITLE OF INVENTION: Polynucleotide Encoding Members of the Human B Cell Antigen Receptor
 TITLE OF INVENTION: Polynucleotide Encoding Members of the Human B Cell Antigen Receptor
 NUMBER OF SEQUENCES: 65
 CORRESPONDENCE ADDRESS: COOKFIELD
 STREET: 60 State Street, suite 510
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02109-1875
 COMPUTER READABLE FORM: disk
 COMPUTER: IBM PC compatible


```

1  COMPUTER: IBM PC compatible
2  OPERATING SYSTEM: PC-DOS/MS-DOS
3  CURFRAMES: Patent in Release #1.0, Version #1.25
4  APPLICATION NUMBER: US/08/456 104
5  CLASSIFICATION: C24
6  PRIOR APPLICATION DATA:
7  APPLICATION NUMBER: 08/101,624;
8  FILING DATE: 26-JUL-1994
9  FILING DATE: 26-JUL-1993
10 APPLICATION NUMBER: 19-AUG-1993
11 ATTORNEY/AGENT INFORMATION:
12 REFERENCE/DOCKET NUMBER: RPI-008
13 REGISTRATION NUMBER: 36 207
14 TELEPHONE: (617) 227-5941
15 TELEFAX: (617) 227-5941
16 INFORMATION FOR SEQ ID NO: 4:
17 TYPE: amino acid
18 LENGTH: 309 amino acids
19 MOLECULE TYPE: protein
20 US-08-456-104-4

```

```

Query Match      42.9%; Score 743.5; DB 2; Length 309;
Best Local Similarity 51.5%; Pred. No. 1.3e-61;
Matches 159; Conservative 45; Mismatches 91; Indels 13; Gaps 5;

```

```

Oy 1 MDPOCTGSLNLPFWALFGLGAPLQAYFNETAIDLPQFANSQNSLSLWVMDQ 60
Db 1 MDPOCTGSLNLPFWALFGLGAPLQAYFNETAIDLPQFANSQNSLSLWVMDQ 60
Oy 61 ENLVNEVLKSEKFSVHSKNGRTSDSVTLRHNLQIKDGLVQCIHHKFTQM 120
Db 61 ENLVNEVLKSEKFSVHSKNGRTSDSVTLRHNLQIKDGLVQCIHHKFTQM 120
Oy 61 QULVETHTGECGLSNYANLQSTDPNNMLRLNVLQIKDGLVQCIHHKFTQM 120
Db 61 QULVETHTGECGLSNYANLQSTDPNNMLRLNVLQIKDGLVQCIHHKFTQM 120
Oy 121 IRHQMSELSVLANSFQRPVLSINTENVYINTCSHYGVPKNSVLRTNSTI 180
Db 121 IRHQMSELSVLANSFQRPVLSINTENVYINTCSHYGVPKNSVLRTNSTI 180
Oy 181 ETCINQCNQVETLVDVSLSPDPVDSMTFTCLTDLTKALLSPFLEDPQ 240
Db 181 ETCINQCNQVETLVDVSLSPDPVDSMTFTCLTDLTKALLSPFLEDPQ 240
Oy 179 EYGMQGLQCNVETLVDVSLSPDPVDSMTFTCLTDLTKALLSPFLEDPQ 238
Db 179 EYGMQGLQCNVETLVDVSLSPDPVDSMTFTCLTDLTKALLSPFLEDPQ 238
Oy 241 PPDHPIK--TAVLPVTCVCKVFLIHWKPKNSYKCNPKYCNHREBSQTKR 298
Db 241 PPDHPIK--TAVLPVTCVCKVFLIHWKPKNSYKCNPKYCNHREBSQTKR 298
Oy 239 P---QTYWHEITAVTALLML--LIIVCHKPKQFQRP---SNTASKLSDNADR 289
Db 239 P---QTYWHEITAVTALLML--LIIVCHKPKQFQRP---SNTASKLSDNADR 289
Oy 299 EKTHIPE 305
Db 299 EKTHIPE 306
Oy 290 ETKINKE 296
Db 290 ETKINKE 296

```

```

RESULT 15 US-08-456-104-23
US-08-456-104-23
Sequence 23, Application US/08479444
Patent No. 6084067
GENERAL INFORMATION:
APPLICANT: Nadel, Lee M.
APPLICANT: Nadel, Lee M.
APPLICANT: Gray, Gary S.
TITLE OF INVENTION: Ligand for Cytokine Receptor
TITLE OF INVENTION: Ligand for Cytokine Receptor
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS: COCKFIELD, LLP
CORRESPONDENCE ADDRESS: COCKFIELD, LLP
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA

```

```

1  ZIP: 02109
2  COMPUTER READABLE FORM:
3  MEDIUM TYPE: floppy disk
4  CURFRAMES: Patent in Release #1.0, Version #1.25
5  OPERATING SYSTEM: PC-DOS/MS-DOS
6  APPLICATION NUMBER: US/08/479 744A
7  CLASSIFICATION: C24
8  PRIOR APPLICATION DATA:
9  APPLICATION NUMBER: 08/280 757
10 FILING DATE: 26-JUL-1994
11 FILING DATE: 26-JUL-1993
12 APPLICATION NUMBER: 19-AUG-1993
13 ATTORNEY/AGENT INFORMATION:
14 REFERENCE/DOCKET NUMBER: RPI-004CP3
15 REGISTRATION NUMBER: 36 207
16 TELEPHONE: (617) 227-5941
17 TELEFAX: (617) 227-5941
18 INFORMATION FOR SEQ ID NO: 23:
19 TYPE: amino acid
20 LENGTH: 309 amino acids
21 MOLECULE TYPE: protein
22 US-08-479-744A-23

```

```

Query Match      42.9%; Score 743.5; DB 3; Length 309;
Best Local Similarity 51.5%; Pred. No. 1.3e-61;
Matches 159; Conservative 45; Mismatches 91; Indels 13; Gaps 5;

```

```

Oy 1 MDPOCTGSLNLPFWALFGLGAPLQAYFNETAIDLPQFANSQNSLSLWVMDQ 60
Db 1 MDPOCTGSLNLPFWALFGLGAPLQAYFNETAIDLPQFANSQNSLSLWVMDQ 60
Oy 61 ENLVNEVLKSEKFSVHSKNGRTSDSVTLRHNLQIKDGLVQCIHHKFTQM 120
Db 61 ENLVNEVLKSEKFSVHSKNGRTSDSVTLRHNLQIKDGLVQCIHHKFTQM 120
Oy 61 QULVETHTGECGLSNYANLQSTDPNNMLRLNVLQIKDGLVQCIHHKFTQM 120
Db 61 QULVETHTGECGLSNYANLQSTDPNNMLRLNVLQIKDGLVQCIHHKFTQM 120
Oy 121 IRHQMSELSVLANSFQRPVLSINTENVYINTCSHYGVPKNSVLRTNSTI 180
Db 121 IRHQMSELSVLANSFQRPVLSINTENVYINTCSHYGVPKNSVLRTNSTI 180
Oy 181 ETCINQCNQVETLVDVSLSPDPVDSMTFTCLTDLTKALLSPFLEDPQ 240
Db 181 ETCINQCNQVETLVDVSLSPDPVDSMTFTCLTDLTKALLSPFLEDPQ 240
Oy 179 EYGMQGLQCNVETLVDVSLSPDPVDSMTFTCLTDLTKALLSPFLEDPQ 238
Db 179 EYGMQGLQCNVETLVDVSLSPDPVDSMTFTCLTDLTKALLSPFLEDPQ 238
Oy 241 PPDHPIK--TAVLPVTCVCKVFLIHWKPKNSYKCNPKYCNHREBSQTKR 298
Db 241 PPDHPIK--TAVLPVTCVCKVFLIHWKPKNSYKCNPKYCNHREBSQTKR 298
Oy 239 P---QTYWHEITAVTALLML--LIIVCHKPKQFQRP---SNTASKLSDNADR 289
Db 239 P---QTYWHEITAVTALLML--LIIVCHKPKQFQRP---SNTASKLSDNADR 289
Oy 299 EKTHIPE 305
Db 299 EKTHIPE 306
Oy 290 ETKINKE 296
Db 290 ETKINKE 296

```

```

Search completed: February 13, 2003, 11:33:51
Job time : 14.9918 secs

```


RESULT 5

B-lymphocyte activation antigen 7 precursor - mouse

C Species: Mus musculus (house mouse)

R-Judge: T.A., Liu, M., Christensen, P.J., Pak, J.J., Turks, L.A.

A-Title: Cloning the rat homolog of the CD26/CD145 ligand B7-1, structural and function

A-Reference number: 145766; MID:9525184; PMID:733533

A-Accession: 145766

A-Molecule type: mRNA

A-Residues: 1-321 <RES>

A-Superfamily: B-lymphocyte restricted antigen B7

Query Match Similarity 13 94; Score 223; DB 2; Length 321;

Matches 78; Conservative 51; Mismatches 117; Indels 58; Gaps 13;

Qy 9 DALIITVLLISDAVSIVTQVNTVTCSPKANKATLSLWVQVQVUULV 65

Db 24 LPVLLVGLAIGISIVQVQKVKELKSLCYFCEGSEIIR---ITWQIDWNL 79

Qy 66 VEYVLEKLSLVNKKYLTSTSDPNNVTLRLHVLKQMSVCTQKPPSTILIQ 124

Db 80 SV-----ISGVFVPMKIVNTVYDINNVSTFSLGLSLDRITTCVQVYDQGVYVNR 135

Qy 125 VITVTLVSNFSEPIKLAQVNT---QNSGIDN---LTKSGQKPKVWVQVYVNR 179

Db 136 IYVTLVSNFVADPPT---NITEGSPADITGTCFASQCFPELHSL---LNGREL 187

Qy 180 YGNNQISQVNTVSTSNLSLSPFQGVVMTVVCLETSEKSKPLFTQEP--- 237

Db 188 GNTITTSQDSSESLITSSQLQF---NNTDFDTETGIDQVAGQ---NFTWVPE 241

Qy 238 ----SQP-----YMKETASVTALLVALLIV---CHKENQPS 272

Db 242 DPBEKQVTPNAGQVAKVLIPIFALIVIVIAIAIATLIFCTVETFRFTRNDAS 301

Qy 273 RSN 276

Db 302 RSTN 305

RESULT 7

C58 precursor - rabbit

C Species: Capra hircus (domestic rabbit)

R-Judge: T.A., Liu, M., Christensen, P.J., Pak, J.J., Turks, L.A.

A-Title: Cloning and sequencing of the rabbit gene encoding T-cell costimulatory molecule

A-Reference number: 146690; MID:95368849; PMID:7442224

A-Accession: 146690

A-Molecule type: mRNA

A-Residues: 1-217 <RES>

A-Superfamily: B-lymphocyte restricted antigen B7

Query Match Similarity 12 217-220, 1995

Matches 85; Conservative 58; Mismatches 111; Indels 67; Gaps 19;

Qy 3 PACT-NEALITPVLLISDAVSIVTQVNTVTCSPKANKATLSLWVQVQVUULV 58

Db 12 PACT-NEALITPVLLISDAVSIVTQVNTVTCSPKANKATLSLWVQVQVUULV 58

Qy 59 DQKLVYBIEHLEKLSLV---VNAKLTGTFEP-RNNTVRLHVLKQMSVCTQK 113

Db 67 KQVQV-----SILSQVETWESIKMTFPIINILNLSLALADQVITTCVQ 118

Qy 111 KPTPTSTLIQQLTLESLVNFSPSEPKLAQNTQSGIN---LTTCTQKQFENQ 169

Db 111 KPTPTSTLIQQLTLESLVNFSPSEPKLAQNTQSGIN---LTTCTQKQFENQ 169

RESULT 6

B-lymphocyte activation antigen 7 precursor - rat

C Species: Rattus norvegicus (Norway rat)

R-Judge: T.A., Liu, M., Christensen, P.J., Pak, J.J., Turks, L.A.

A-Title: Cloning the rat homolog of the CD26/CD145 ligand B7-1, structural and function

A-Reference number: 145766; MID:9525184; PMID:733533

A-Accession: 145766

A-Molecule type: mRNA

A-Residues: 1-321 <RES>

A-Superfamily: B-lymphocyte restricted antigen B7

Query Match Similarity 14 44; Score 231; DB 2; Length 309;

Matches 85; Conservative 52; Mismatches 127; Indels 50; Gaps 12;

Qy 11 TLPIITVLLISDAVSIVTQVNTVTCSPKANKATLSLWVQVQVUULV 67

Db 28 IYVTLVSNFVADPPT---NITEGSPADITGTCFASQCFPELHSL---LNGREL 187

Qy 66 VEYVLEKLSLVNKKYLTSTSDPNNVTLRLHVLKQMSVCTQKPPSTILIQ 124

Db 79 -----SVYGLKQVETVNTVYDINNVSTFSLGLSLDRITTCVQVYDQGVYVNR 135

Qy 121 ILIQTTLVSNFSEPIKLAQNTQSGINLTKSGQKPKVWVQVYVNR 179

Db 130 EVGLVLAIGISIVQVQKVKELKSLCYFCEGSEIIR---ITWQIDWNL 79

Qy 181 COMQVSDVNTVSTSNLSLSPFQGVVMTVVCLETSEKSKPLFTQEP--- 237

Db 187 GNTITTSQDSSESLITSSQLQF---NNTDFDTETGIDQVAGQ---NFTWVPE 241

Qy 238 ----SQP-----YMKETASVTALLVALLIV---CHKENQPS 272

Db 242 DPBEKQVTPNAGQVAKVLIPIFALIVIVIAIAIATLIFCTVETFRFTRNDAS 301

Qy 273 RSN 276

Db 302 RSTN 305

RESULT 6

B-lymphocyte activation antigen 7 precursor - rat

C Species: Rattus norvegicus (Norway rat)

R-Judge: T.A., Liu, M., Christensen, P.J., Pak, J.J., Turks, L.A.

A-Title: Cloning the rat homolog of the CD26/CD145 ligand B7-1, structural and function

A-Reference number: 145766; MID:9525184; PMID:733533

A-Accession: 145766

A-Molecule type: mRNA

A-Residues: 1-321 <RES>

A-Superfamily: B-lymphocyte restricted antigen B7

Query Match Similarity 14 44; Score 231; DB 2; Length 309;

Matches 85; Conservative 52; Mismatches 127; Indels 50; Gaps 12;

Qy 11 TLPIITVLLISDAVSIVTQVNTVTCSPKANKATLSLWVQVQVUULV 67

Db 28 IYVTLVSNFVADPPT---NITEGSPADITGTCFASQCFPELHSL---LNGREL 187

DR P1am: P00047; qg: 2;
 DR SMART: SM00410; IG like: 1;
 DR SMART: SM00416; GOV: 1;
 KM Immunoglobulin domain; Signal, Antigen.
 KM Transmembrane; Signal, Antigen.
 FT SIGNAL 1 21
 FT DOMAIN 22 239
 FT TRANSFER 236 256
 FT CYTOPLASMIC 1 (POTENTIAL)
 FT DOMAIN 237 329
 FT DOMAIN 139 229
 FT DOMAIN 139 229
 FT POLY-CYS. 258 261
 FT DISULFID 146 222
 FT DISULFID 162 211
 FT DISULFID 162 211
 FT N-LINKED GLYC. (POTENTIAL)
 FT N-LINKED GLYC. (POTENTIAL)
 FT CARBOHYD 200 200
 FT CARBOHYD 223 223
 SQ SEQUENCE 319 AA; 35632 MW, 98FC7AF45C2408E C164;
 Query Match
 Best local similarity 24.5%; Pred. No. 0.0016;
 Matches 95; Conservative 47; Mismatches 109; Indels 89; Gaps 19;
 Qy 15 VTLASLGVSEVST---QAVNTGVLPCFPAQN-----ISLSLGVFV 57
 Db 17 VLV---GLSVLTQVQLAQGVSTVYTHYSISREGLQKQKLLKLVITV 72
 Qy 58 QQQQLVLYVETKELGVSAVYKLTGFSPN---NMTLRUNVQIKMGSTCFQ 113
 Db 73 PFENK---NYHCE-----LYKVRVSNNAQSGASTITQLTWDVDTIC 117
 Qy 114 KPPFGGIIQQLT---TELVATSESPK-AQNTGNSGIMLTCTKQHPK 165
 Db 118 ---SVSLMDGENTKSRVLLVPSFPGEGEETLQNLQUTQKHSPT 170
 Qy 156 PK---KNVELTNSGDMQVIGQVETSTPSISGLSGLSPGQVMTVWVLES 224
 Db 171 PVSMTV---MIHQQLAPASQVPLKNSIDTS---GY---LTS 214
 Qy 223 WLSSKPNATQFESQ---TYKMTASTVALLVLLVCHVKVQPSRSTAS 279
 Db 215 MEDGFCNTVAFSPGNVALVGVGVVALLIIGIIVCCCR---GDGNTD 270
 Qy 260 KLESDNADRTI---NKLK 297
 Db 271 K-EDAPNATVPPQKQL 291
 RESUME 10
 SLAM MOUSE
 ID SLAM MOUSE STANDARD; PRT: 343 AA.
 AC QPQMA; 09QX23; 148; Creted;
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 GN Slammap: lymphocytic activation molecule precursor.
 OS Mus musculus (Mouse).
 CC Baktayora; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Oryzias latipes; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI TaxId=10096;
 RN [1] JENSEN FROM N.A. (LONG AND SHORT ISOFORMS).
 RC MEDLINE=20040317; PubMed=10574270;
 RA Castro A.G., Hauser T.W., Cocks B.G., Abrams J., Zuraevsk S.,
 RA Nichols K.B., de Vries J.F., Janier L., Luyt O., Gstra
 RT Molecular and functional characterization of mouse signaling
 RT lymphocytic activation molecule (SLAM): differential expression and
 RT responsiveness in th1 and th2 cells.;

RL [2] Immunol. 143; 5860-5870 (1999).
 RL SEQUENCE FROM N.A. (LONG ISOFORM).
 RL Wang M., Wu C., Seyoum O., Terhorst C.,
 Submitted (Jul-1999) to the EMBL/Genbank/DBJ databases.
 CC FUNCTION: HIGH-AFFINITY SELF-LIGAND CONSIDERED TO BE IMPORTANT IN
 CC TRANSFORMATION EVENTS IN T LYMPHOCYTES ARE DIFFERENT FROM THOSE IN B
 CC CELLS. TWO MODES OF SLAM SIGNALING ARE LIKELY TO EXIST: ONE IN B
 CC ANOTHER IN WHICH PROTEIN TYROSINE KINASES A NEGATIVE REGULATOR AND
 CC DEPENDENT SIGNAL TRANSDUCTION OPERATES.
 CC SUBUNIT: ITS CYTOPLASMIC DOMAIN INTERACTS WITH SH2 DOMAIN PROTEIN
 CC PHOSPHATASE WITH PTEN1, BUT NOT WITH SHP-1.
 CC SUBCELLULAR LOCATION: TYPE 1 MEMBRANE PROTEIN. PRESENT ON THE
 CC PLASMA MEMBRANE OF T LYMPHOCYTES.
 CC ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
 CC SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC SIMILARITY: PHOSPHORYLATED TO THE IMMUNOGLOBULIN SUPRAMILY.
 CC SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C-TYPE DOMAIN.
 CC This EMIS: PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC at the European Bioinformatics Institute. There are no restrictions on its
 CC use, but the EMIS logo must be present on all copies. The EMIS logo may be
 CC modified and this statement is not removed. Usage by for commercial
 CC entities requires a license agreement (see <http://www.ebi.ac.uk/comm/usage/>)
 CC -----o licensed-asib-sib.ch)-----
 DR EMBL; AF145791; AAF22211.1;
 DR EMBL; AF145792; AAF22212.1;
 DR EMBL; AF145793; AAF22213.1;
 DR EMBL; AF146619; AAF13818.1; JOINED
 DR EMBL; AF146620; AAF13818.1; JOINED
 DR EMBL; AF146621; AAF13818.1; JOINED
 DR EMBL; AF146622; AAF13818.1; JOINED
 DR EMBL; AF160990; AAF14535.1;
 DR EMBL; AF160991; AAF14535.1;
 KM Receptor; Signal; Transmembrane; T-cell; Glycoprotein; Repeat.
 KM Immunoglobulin domain; Phosphorylation; Alternative splicing.
 FT SIGNAL 1 24
 FT SIGNAL 25 343
 FT DOMAIN 25 242
 FT CYTOPLASMIC 243 343
 FT CYTOPLASMIC 243 343
 FT CYTOPLASMIC 243 343
 FT IG-LIKE V-TYPE DOMAIN.
 FT IG-LIKE C-TYPE DOMAIN.
 FT BY SIMILARITY.
 FT DISULFID 167 212
 FT SITE 286 291
 FT SITE 333 338
 FT SH2-BINDING (POTENTIAL).
 FT SH2-BINDING (POTENTIAL).
 FT SH2-BINDING (POTENTIAL).
 FT CARBOHYD 54 54
 FT CARBOHYD 139 103
 FT CARBOHYD 139 103
 FT CARBOHYD 136 126
 FT CARBOHYD 151 151
 FT CARBOHYD 151 151
 FT CARBOHYD 192 192
 FT CARBOHYD 211 211
 FT CARBOHYD 226 226
 FT VAREPLIC 226 343
 SQ SEQUENCE 343 AA; 38094 MW; 798607151B334C1 C64;
 Query Match
 Best local similarity 8.1%; Score 129.5; DB 1; Length 343;
 Best local similarity 20.9%; Pred. No. 0.0036;

CC	This SWISS-PROT entry is copyright. It is produced through a collaboration	
CC	between the European Bioinformatics Institute, the Swiss Institute for	
CC	the European Bioinformatics Institute. There are no restrictions on its	
CC	use by non-profit institutions as long as its content is not used in any	
CC	way that might be considered to be derogatory to the EMBL, EBI or	
CC	modified and this statement is not removed (see http://www.isb-sib.ch/announce/	
CC	or send an email to license@isb-sib.ch)	
CC	PIR: A60355; A60356; A60357; A60358; A60359; A60360; A60361; A60362; A60363; A60364; A60365; A60366; A60367; A60368; A60369; A60370; A60371; A60372; A60373; A60374; A60375; A60376; A60377; A60378; A60379; A60380; A60381; A60382; A60383; A60384; A60385; A60386; A60387; A60388; A60389; A60390; A60391; A60392; A60393; A60394; A60395; A60396; A60397; A60398; A60399; A60400; A60401; A60402; A60403; A60404; A60405; A60406; A60407; A60408; A60409; A60410; A60411; A60412; A60413; A60414; A60415; A60416; A60417; A60418; A60419; A60420; A60421; A60422; A60423; A60424; A60425; A60426; A60427; A60428; A60429; A60430; A60431; A60432; A60433; A60434; A60435; A60436; A60437; A60438; A60439; A60440; A60441; A60442; A60443; A60444; A60445; A60446; A60447; A60448; A60449; A60450; A60451; A60452; A60453; A60454; A60455; A60456; A60457; A60458; A60459; A60460; A60461; A60462; A60463; A60464; A60465; A60466; A60467; A60468; A60469; A60470; A60471; A60472; A60473; A60474; A60475; A60476; A60477; A60478; A60479; A60480; A60481; A60482; A60483; A60484; A60485; A60486; A60487; A60488; A60489; A60490; A60491; A60492; A60493; A60494; A60495; A60496; A60497; A60498; A60499; A60500; A60501; A60502; A60503; A60504; A60505; A60506; A60507; A60508; A60509; A60510; A60511; A60512; A60513; A60514; A60515; A60516; A60517; A60518; A60519; A60520; A60521; A60522; A60523; A60524; A60525; A60526; A60527; A60528; A60529; A60530; A60531; A60532; A60533; A60534; A60535; A60536; A60537; A60538; A60539; A60540; A60541; A60542; A60543; A60544; A60545; A60546; A60547; A60548; A60549; A60550; A60551; A60552; A60553; A60554; A60555; A60556; A60557; A60558; A60559; A60560; A60561; A60562; A60563; A60564; A60565; A60566; A60567; A60568; A60569; A60570; A60571; A60572; A60573; A60574; A60575; A60576; A60577; A60578; A60579; A60580; A60581; A60582; A60583; A60584; A60585; A60586; A60587; A60588; A60589; A60590; A60591; A60592; A60593; A60594; A60595; A60596; A60597; A60598; A60599; A60600; A60601; A60602; A60603; A60604; A60605; A60606; A60607; A60608; A60609; A60610; A60611; A60612; A60613; A60614; A60615; A60616; A60617; A60618; A60619; A60620; A60621; A60622; A60623; A60624; A60625; A60626; A60627; A60628; A60629; A60630; A60631; A60632; A60633; A60634; A60635; A60636; A60637; A60638; A60639; A60640; A60641; A60642; A60643; A60644; A60645; A60646; A60647; A60648; A60649; A60650; A60651; A60652; A60653; A60654; A60655; A60656; A60657; A60658; A60659; A60660; A60661; A60662; A60663; A60664; A60665; A60666; A60667; A60668; A60669; A60670; A60671; A60672; A60673; A60674; A60675; A60676; A60677; A60678; A60679; A60680; A60681; A60682; A60683; A60684; A60685; A60686; A60687; A60688; A60689; A60690; A60691; A60692; A60693; A60694; A60695; A60696; A60697; A60698; A60699; A60700; A60701; A60702; A60703; A60704; A60705; A60706; A60707; A60708; A60709; A60710; A60711; A60712; A60713; A60714; A60715; A60716; A60717; A60718; A60719; A60720; A60721; A60722; A60723; A60724; A60725; A60726; A60727; A60728; A60729; A60730; A60731; A60732; A60733; A60734; A60735; A60736; A60737; A60738; A60739; A60740; A60741; A60742; A60743; A60744; A60745; A60746; A60747; A60748; A60749; A60750; A60751; A60752; A60753; A60754; A60755; A60756; A60757; A60758; A60759; A60760; A60761; A60762; A60763; A60764; A60765; A60766; A60767; A60768; A60769; A60770; A60771; A60772; A60773; A60774; A60775; A60776; A60777; A60778; A60779; A60780; A60781; A60782; A60783; A60784; A60785; A60786; A60787; A60788; A60789; A60790; A60791; A60792; A60793; A60794; A60795; A60796; A60797; A60798; A60799; A60800; A60801; A60802; A60803; A60804; A60805; A60806; A60807; A60808; A60809; A60810; A60811; A60812; A60813; A60814; A60815; A60816; A60817; A60818; A60819; A60820; A60821; A60822; A60823; A60824; A60825; A60826; A60827; A60828; A60829; A60830; A60831; A60832; A60833; A60834; A60835; A60836; A60837; A60838; A60839; A60840; A60841; A60842; A60843; A60844; A60845; A60846; A60847; A60848; A60849; A60850; A60851; A60852; A60853; A60854; A60855; A60856; A60857; A60858; A60859; A60860; A60861; A60862; A60863; A60864; A60865; A60866; A60867; A60868; A60869; A60870; A60871; A60872; A60873; A60874; A60875; A60876; A60877; A60878; A60879; A60880; A60881; A60882; A60883; A60884; A60885; A60886; A60887; A60888; A60889; A60890; A60891; A60892; A60893; A60894; A60895; A6089	

[illegible]

CY 266 ----FNQPSFNTAKLENNMAD 268
DB 265 GYFSEKTSFOKNSSSKATTMSND 269

Search completed: February 13, 2003, 11:31:41
Job time : 18:4671 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 13, 2003, 11:28:39 : Search time 27.6066 Seconds
2306.282 Million cell updates/sec
(Without alignments)

Title: US-09-425-516-23

Perfect score: 1599
Sequence: 1 MDPCTGLIALIFVTVLLI.....ETINMELERQIAAFANF 309

Scoring table: BLOSUM62

Gap: 10.0, Gapext 0.5

Searched: 671580 seqs, 206069115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 10%

Displaying first 10 summaries

Database :

1: SPREMGL_21.*
2: SP_bacteria.*
3: SP_fungi.*
4: SP_human.*
5: SP_mammal.*
6: SP_mammal.*
7: SP_mhc.*
8: SP_mhc.*
9: SP_Phage.*
10: SP_plant.*
11: SP_plant.*
12: SP_plant.*
13: SP_vertebrate.*
14: SP_vertebrate.*
15: SP_vertebrate.*
16: SP_bacteriopl.*
17: SP_archaeop.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB ID	Description
1	1578	98.7	309	11	Q91V77	Q91V77 mus musculus
2	1579	98.7	309	11	Q91V77	Q91V77 mus musculus
3	1587	98.0	356	11	Q64381	Q64381 mus musculus
4	1027	64.2	333	11	Q35511	Q35511 rattus norv
5	705.5	44.1	333	6	Q91V77	Q91V77 mus musculus
6	705.5	44.1	333	6	Q91V77	Q91V77 mus musculus
7	701.5	43.9	333	6	Q91V77	Q91V77 mus musculus
8	689.5	43.1	333	6	Q91V77	Q91V77 mus musculus
9	689.5	43.1	333	6	Q91V77	Q91V77 mus musculus
10	662	41.4	320	6	Q91V77	Q91V77 mus musculus
11	658	41.2	320	6	Q91V77	Q91V77 mus musculus
12	658	41.2	320	6	Q91V77	Q91V77 mus musculus
13	650.5	40.7	275	6	Q91V77	Q91V77 mus musculus
14	640.5	40.1	339	6	Q91V77	Q91V77 mus musculus
15	640.5	40.1	339	6	Q91V77	Q91V77 mus musculus
16	640.5	40.1	339	6	Q91V77	Q91V77 mus musculus

17 585 16.6 284 6 Q91L33 Q91L33 bos taurus
18 226.5 14.2 306 11 Q91L29 Q91L29 mus musculus
19 223 13.9 321 11 Q91L29 Q91L29 mus musculus
20 223 13.9 321 11 Q91L29 Q91L29 mus musculus
21 215 13.4 321 11 Q91L29 Q91L29 mus musculus
22 210 13.1 316 11 Q91V77 Q91V77 mus musculus
23 180.5 11.3 306 6 Q91V77 Q91V77 mus musculus
24 180.5 11.3 306 6 Q91V77 Q91V77 mus musculus
25 176 11.0 306 6 Q91V77 Q91V77 mus musculus
26 176 11.0 306 6 Q91V77 Q91V77 mus musculus
27 176 11.0 306 6 Q91V77 Q91V77 mus musculus
28 175.5 11.0 292 6 Q91V77 Q91V77 mus musculus
29 175.5 11.0 292 6 Q91V77 Q91V77 mus musculus
30 168 10.5 296 6 Q91V77 Q91V77 mus musculus
31 168 10.5 296 6 Q91V77 Q91V77 mus musculus
32 164.5 10.3 235 6 Q91V77 Q91V77 mus musculus
33 164.5 10.3 235 6 Q91V77 Q91V77 mus musculus
34 163 10.2 334 4 Q91V77 Q91V77 mus musculus
35 163 10.2 334 4 Q91V77 Q91V77 mus musculus
36 163 10.2 334 4 Q91V77 Q91V77 mus musculus
37 160.5 10.0 288 6 Q91V77 Q91V77 mus musculus
38 160.5 10.0 288 6 Q91V77 Q91V77 mus musculus
39 156 9.8 229 6 Q91V77 Q91V77 mus musculus
40 156 9.8 229 6 Q91V77 Q91V77 mus musculus
41 156 9.8 229 6 Q91V77 Q91V77 mus musculus
42 148.5 9.3 220 4 Q91V77 Q91V77 mus musculus
43 148.5 9.3 220 4 Q91V77 Q91V77 mus musculus
44 148.5 9.3 220 4 Q91V77 Q91V77 mus musculus
45 144.5 9.0 289 6 Q91V77 Q91V77 mus musculus

ALIGNMENTS

RESULT 1
Q91V77
ID Q91V77 PRELIMINARY: PRF: 309 AA.
DB Q91V77
Q91V77 DEC-2001 (Trembl, 19, Created)
DT 01-DEC-2001 (Trembl, 19, Last sequence update)
DT 01-JUN-2002 (Trembl, 21, Last annotation update)
GN Q91V77
GN CD86
OS Mus musculus (Mouse)
OS NCBI_TaxID:10090;
OX NCBI_TaxID:10090;
OX NCBI_TaxID:10090;
OX NCBI_TaxID:10090;
RA Strauberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL:AF18897.1;
DR GenBank:U00107.1;
DR DDBJ:U00107.1;
SQ SEQUENCE 309 AA: 34714 MW: 61593.045EFCEBCEZ CRC64;

Query Match 98.7% Score 1579; DB 11; Length 309;
Best Local Similarity 98.0%; Pred. No. 4, re-129;
Matches 36; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 MDPCTGLIALIFVTVLLISDAVSVEQATPGTALPCPTKAQISLSELPVQDQ 60
Db 1 MDPCTGLIALIFVTVLLISDAVSVEQATPGTALPCPTKAQISLSELPVQDQ 60
Qy 61 QKVLVETLITGLKLSNNKYGTSFDNNATLVNUNVQKMGVSCFQKQPTGS 120
Db 61 QKVLVETLITGLKLSNNKYGTSFDNNATLVNUNVQKMGVSCFQKQPTGS 120
Qy 121 IIQQLTVELVANSFPEIKLAQNTGSSGINTTSCQKPKPKQKQVLTINSTEY 180
Db 121 IIQQLTVELVANSFPEIKLAQNTGSSGINTTSCQKPKPKQKQVLTINSTEY 180
Qy 181 GDMVQSDNNITFLSINLSISLSPDQVMTVVCLETENKISKLMFTPTSPSQ 240
Db 181 GDMVQSDNNITFLSINLSISLSPDQVMTVVCLETENKISKLMFTPTSPSQ 240

Qy 240 ---OTYKELTASVYALLVLLVLLV-----HWKNDQSSSH--FACKLER-D 284
 Db 243 DQDHLH-----IAALLW-LVLLVVFLLRKKKKQGF-FSECKTINKEKE 292
 Qy 285 SNADESTINLEL 298
 Db 293 SOTVETVETHS 306
 RESULT 9
 ID Q98D96 PRELIMINARY; PRT: 323 AA.
 AC Q98D96: 2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 OS C66 protein precursor (called macrop)
 OC C66 protein precursor (called macrop)
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Buthera; Primates; Carnivora; Cercopitheidae;
 CC NCBI TaxID=9645; Macaca.
 RN [1]--Faint=9645;
 RP SEQUENCE FROM N.A. PubMed=1491535.
 RA Villinger F., Beak P., Mayne A.E., King C.L., Genain C.P.,
 RA Weiss M.R., Anari M.A.; J. Neurology analysis of nonhuman primate
 RL FGF19 and its homologous molecules;
 RL Immunogenetics 53:315-328(2001).
 DR EMBL: AF344851; AAC37611.1; .
 DR SMART: SM00409; IG. 1.
 DR InterPro: IPR003596; IG. v.
 KW Signal; SM00406; IG. 1.
 FT SIGNAL 1 17 POTENTIAL.
 SQ SEQUENCE 323 AA; 37079 MW, 60682PZ5C67FD CRC64;
 Query Match 43.1%; Score 689.5; DB 6; Length 323;
 Best Local Similarity 50.5%; Pred. No. 8; e-52;
 Matches 142; Conservative 41; Mismatches 95; Indels 13; Gaps 5;
 Qy 7 MGLALITPVLLIDANSVETQVNFATLCPPTKAGNI-SLELVFMDQQLVLY 66
 Db 1 MGLALITPVLLIDANSVETQVNFATLCPPTKAGNI-SLELVFMDQQLVLY 60
 Qy 67 EYLTGELDSVWATLSPDRNWTLLRVNVLQKNGSTCFQKPTGFTLLQOT 126
 Db 61 EYLTGQEPHNSVKTMTGTFSTQATWTLRVNVLQKNGSTCFQKPTGFTLLQOT 120
 Qy 127 LTELGVANFSPERIKLAQNPQNGINATKQKQKQKQKFLT--NRYEYGDGM 184
 Db 121 LTELGVANFSPERIKLAQNPQNGINATKQKQKQKQKFLT--NRYEYGDGM 180
 Qy 185 QLSQNDVTELSINSLSPGPPQVNVVTVLSTENK--LSKRLFTQSTPQTY 242
 Db 181 KSDQNTNTELVNINSLSPGPPET--NVSIVQLQSPKTLPSLQPCDAPVPPV 239
 Qy 243 KSEITASVYALLVLLVLLV-----HWKNDQSSSH--FACKLER-D 292
 Db 240 DQDHLH-----IAALLW-LVLLVVFLLRKKKKQGF-FSECKTINKEKE 295
 Qy 294 LKLELQASAK 305
 Db 296 LKLELQASAK 307
 RESULT 11
 ID Q9TTF1 PRELIMINARY; PRT: 280 AA.
 AC Q9TTF1: 2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 OS Chondrichthyes; Buthera; Chordata; Vertebrata; Euteleostomi;
 CC Buthera; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Buthera; Chondrichthyes; Chondrichthyes; Chondrichthyes;
 CC NCBI TaxID=9645;
 RN [1]--Faint=9645;
 RP SEQUENCE FROM N.A. PubMed=1063000;
 RA Yang S.-S., Kim G.-K.;
 RL New forms of Dog CD80 and CD86 Transcripts that Encode Secreted 87
 RL Immunogenetics 50:349-353(1999).
 DR EMBL: AF106827; AAF1298.1; .
 KW BNP; P33681; 1099.
 FT BNP 1099
 SQ SEQUENCE 280 AA; 30709 MW, 60682PZ5C67FD CRC64;
 Query Match 43.1%; Score 689.5; DB 6; Length 323;
 Best Local Similarity 50.5%; Pred. No. 8; e-52;
 Matches 142; Conservative 41; Mismatches 95; Indels 13; Gaps 5;
 Qy 7 MGLALITPVLLIDANSVETQVNFATLCPPTKAGNI-SLELVFMDQQLVLY 66
 Db 1 MGLALITPVLLIDANSVETQVNFATLCPPTKAGNI-SLELVFMDQQLVLY 60
 Qy 67 EYLTGELDSVWATLSPDRNWTLLRVNVLQKNGSTCFQKPTGFTLLQOT 126
 Db 61 EYLTGQEPHNSVKTMTGTFSTQATWTLRVNVLQKNGSTCFQKPTGFTLLQOT 120
 Qy 127 LTELGVANFSPERIKLAQNPQNGINATKQKQKQKQKFLT--NRYEYGDGM 184
 Db 121 LTELGVANFSPERIKLAQNPQNGINATKQKQKQKQKFLT--NRYEYGDGM 180
 Qy 185 QLSQNDVTELSINSLSPGPPQVNVVTVLSTENK--LSKRLFTQSTPQTY 242
 Db 181 KSDQNTNTELVNINSLSPGPPET--NVSIVQLQSPKTLPSLQPCDAPVPPV 239
 Qy 243 KSEITASVYALLVLLVLLV-----HWKNDQSSSH--FACKLER-D 292
 Db 240 DQDHLH-----IAALLW-LVLLVVFLLRKKKKQGF-FSECKTINKEKE 295
 Qy 294 LKLELQASAK 305
 Db 296 LKLELQASAK 307
 RESULT 10
 ID Q02816 PRELIMINARY; PRT: 325 AA.
 AC Q02816: 2001 (TrEMBLrel. 17, Created)
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)

DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE B7-2;
 OS Sus scrofa (pig).
 CC Eukaryota; Metazoa; Chordata; Carnivora; Vertebrata; Euteleostomi;
 CC Mammalia; Buthera; Cetartiodactyla; Suidae; Suidae; Sus.
 CC NCBI TaxID=99823;
 RN [1]--Faint=99823;
 RP SEQUENCE FROM N.A. PubMed=889513.
 RA Meier S., Karmann K., Min M., Hughes C.C., Pober J.S.,
 RA Bethwell A.L.;
 RL Celline Chondrichthyes CD86 is a major costimulator of xenogeneic human
 RL endothelial cells;
 RL J Immunol. 157:3838-3844(1996).
 DR EMBL: U000556; IG. v.
 DR InterPro: IPR003596; IG. v.
 DR SMART: SM00406; IG. 1.
 SQ SEQUENCE 325 AA; 36527 MW, 98858B017B057D CRC64;
 Query Match 41.4%; Score 662; DB 6; Length 325;
 Best Local Similarity 45.5%; Pred. No. 2; e-49;
 Matches 142; Conservative 57; Mismatches 95; Indels 18; Gaps 6;
 Qy 7 MGLALITPVLLIDANSVETQVNFATLCPPTKAGNI-SLELVFMDQQLVLY 66
 Db 1 MGLALITPVLLIDANSVETQVNFATLCPPTKAGNI-SLELVFMDQQLVLY 60
 Qy 67 EYLTGELDSVWATLSPDRNWTLLRVNVLQKNGSTCFQKPTGFTLLQOT 126
 Db 61 EYLTGQEPHNSVKTMTGTFSTQATWTLRVNVLQKNGSTCFQKPTGFTLLQOT 120
 Qy 127 LTELGVANFSPERIKLAQNPQNGINATKQKQKQKQKFLT--NRYEYGDGM 184
 Db 121 LTELGVANFSPERIKLAQNPQNGINATKQKQKQKQKFLT--NRYEYGDGM 180
 Qy 185 QLSQNDVTELSINSLSPGPPQVNVVTVLSTENK--LSKRLFTQSTPQTY 242
 Db 181 KSDQNTNTELVNINSLSPGPPET--NVSIVQLQSPKTLPSLQPCDAPVPPV 239
 Qy 243 KSEITASVYALLVLLVLLV-----HWKNDQSSSH--FACKLER-D 292
 Db 240 DQDHLH-----IAALLW-LVLLVVFLLRKKKKQGF-FSECKTINKEKE 295
 Qy 294 LKLELQASAK 305
 Db 296 LKLELQASAK 307
 RESULT 11
 ID Q9TTF1 PRELIMINARY; PRT: 280 AA.
 AC Q9TTF1: 2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 OS Chondrichthyes; Buthera; Chordata; Vertebrata; Euteleostomi;
 CC Buthera; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Buthera; Chondrichthyes; Chondrichthyes; Chondrichthyes;
 CC NCBI TaxID=9645;
 RN [1]--Faint=9645;
 RP SEQUENCE FROM N.A. PubMed=1063000;
 RA Yang S.-S., Kim G.-K.;
 RL New forms of Dog CD80 and CD86 Transcripts that Encode Secreted 87
 RL Immunogenetics 50:349-353(1999).
 DR EMBL: AF106827; AAF1298.1; .
 KW BNP; P33681; 1099.
 FT BNP 1099
 SQ SEQUENCE 280 AA; 30709 MW, 60682PZ5C67FD CRC64;
 Query Match 43.1%; Score 689.5; DB 6; Length 323;
 Best Local Similarity 50.5%; Pred. No. 8; e-52;
 Matches 142; Conservative 41; Mismatches 95; Indels 13; Gaps 5;
 Qy 7 MGLALITPVLLIDANSVETQVNFATLCPPTKAGNI-SLELVFMDQQLVLY 66
 Db 1 MGLALITPVLLIDANSVETQVNFATLCPPTKAGNI-SLELVFMDQQLVLY 60
 Qy 67 EYLTGELDSVWATLSPDRNWTLLRVNVLQKNGSTCFQKPTGFTLLQOT 126
 Db 61 EYLTGQEPHNSVKTMTGTFSTQATWTLRVNVLQKNGSTCFQKPTGFTLLQOT 120
 Qy 127 LTELGVANFSPERIKLAQNPQNGINATKQKQKQKQKFLT--NRYEYGDGM 184
 Db 121 LTELGVANFSPERIKLAQNPQNGINATKQKQKQKQKFLT--NRYEYGDGM 180
 Qy 185 QLSQNDVTELSINSLSPGPPQVNVVTVLSTENK--LSKRLFTQSTPQTY 242
 Db 181 KSDQNTNTELVNINSLSPGPPET--NVSIVQLQSPKTLPSLQPCDAPVPPV 239
 Qy 243 KSEITASVYALLVLLVLLV-----HWKNDQSSSH--FACKLER-D 292
 Db 240 DQDHLH-----IAALLW-LVLLVVFLLRKKKKQGF-FSECKTINKEKE 295
 Qy 294 LKLELQASAK 305
 Db 296 LKLELQASAK 307
 RESULT 10
 ID Q02816 PRELIMINARY; PRT: 325 AA.
 AC Q02816: 2001 (TrEMBLrel. 17, Created)
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)


```

DR InterPro: IPR003596, IG, V.
DR SMART: SM00405, I0V, 1.
SQ SEQUENCE 329 AA; 37481 MW; A10621E3C0A08BB CRC64;
Query Match 40.1%; Score 640.5; DB 6; Length 329;
Best Local Similarity 46.1%; Fwd. No. 1,6e-47;
Matches 140; Conservative 54; Mismatches 86; Indels 19; Gaps 8;
Qy 6 TWGLGALLFVTVLLSVLSIAVSVQATVNTATVLCPTFAQNISELVLPQCKLVL 65
Db 7 TWGLSHRTLLVALLGLSSVMSQSYAFNGCLCHTCHTQNISELVLPQCKLVL 66
Qy 66 VYVYIGTEKLDSVNAKYLGRSTFDNNWTLRHNVQIKMGSYDCKFQKPTPTSI110Q 125
Db 67 YEYFGKGNQVHLAKYKATSTFDKNTLADNVQIKMGSYDCKFQKPTPTSI110Q 126
Qy 126 TVEISLVANSPEIKLAQNTQNSG-INUTCTSKQHKPKQKQVFLIT--NSTNEYD 182
Db 127 NSDGLVANSFQPIITVNTENSGIINLTCSIGQTFPQDNTFQNTENSTYTOT 186
Qy 183 INQISQNVTELSINSLSPFQDQVHVTVVYLETSMK-ISKPYLPNTQFFPSQT 241
Db 187 WKQSQNVTELSINSLSPFVPE-ANNVSVFCALQLETLMLLSLPNDAQ---PKD 242
Qy 242 YNKEITASVTALLVALLIIVC-----HKQKQFQRENTASKLERQSNADRET 291
Db 243 KQPEQGHFLTAIVLWV-FVFGQVGSVFLAKKKQKQG-PSHCETIKERKESQQT 299
Search completed: February 13, 2003, 11:32:43
CPU time : 28.6166 sec

```

```

Qy 183 INQISQNVTELSINSLSPFQDQVHVTVVYLETSMK-ISKPYLPNTQFFPSQT 241
Db 187 WKQSQNVTELSINSLSPFVPE-ANNVSVFCALQLETLMLLSLPNDAQ---PKD 242
Qy 242 YNKEITASVTALLVALLIIVC-----HKQKQFQRENTASKLERQSNADRET 291
Db 243 KQPEQGHFLTAIVLWV-FVFGQVGSVFLAKKKQKQG-PSHCETIKERKESQQT 299
Search completed: February 13, 2003, 11:32:43
CPU time : 28.6166 sec

```

```

RESULT 15
Qy 15 QYQWZQYQWZ PRELIMINARY; FMT: 332 AA.
AC QYQWZ;
DR 01-MAR-2001 (TRENBERG, 16, Created)
DR 01-MAR-2001 (TRENBERG, 16, Updated)
DR 01-DEC-2001 (TRENBERG, 19, Last sequence update)
DE 8-Lymphocyte activation antigen B7-2 (CD86)
GN CD86, silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Neomellia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
SN [18],TaxId:9685;
RP SEQUENCE FROM N.A.
EA NWHLINR2648522; PubMed:1029611;
EA Tsumiya Y., Ikeda Y., Mikani T., Takahashi E.,
RT "Molecular cloning of the cDNA encoding the feline B-lymphocyte
activation antigen B7-2 (CD86) homologues which
interact with human CTLA-4";
RU Eur. J. Immunogenet. 27:427-430(2000) .
RU Buehler, M. and Buehler, M. 1998.
DR InterPro: IPR003596, IG, V.
DR SMART: SM00409, I0V, 1.
DR 50 QYQWZQYQWZ PRELIMINARY; FMT: 332 AA; 37812 MW; 672CB83667D1E3C0 CRC64;
Query Match 40.1%; Score 640.5; DB 6; Length 332;
Best Local Similarity 46.1%; Fwd. No. 1,6e-47;
Matches 140; Conservative 54; Mismatches 86; Indels 19; Gaps 8;
Qy 6 TWGLGALLFVTVLLSVLSIAVSVQATVNTATVLCPTFAQNISELVLPQCKLVL 65
Db 7 TWGLSHRTLLVALLGLSSVMSQSYAFNGCLCHTCHTQNISELVLPQCKLVL 66
Qy 66 VYVYIGTEKLDSVNAKYLGRSTFDNNWTLRHNVQIKMGSYDCKFQKPTPTSI110Q 125
Db 67 YEYFGKGNQVHLAKYKATSTFDKNTLADNVQIKMGSYDCKFQKPTPTSI110Q 126
Qy 126 TVEISLVANSPEIKLAQNTQNSG-INUTCTSKQHKPKQKQVFLIT--NSTNEYD 182
Db 127 NSDGLVANSFQPIITVNTENSGIINLTCSIGQTFPQDNTFQNTENSTYTOT 186

```


FT Domain /label= Transmembrane_domain
 FT 266..309
 FT /label= Cytoplasmic_domain
 PN W09640915-A2.
 XX 19-DEC-1996.
 PP 06-JUN-1996; 96W0-1809052.
 PP 07-JUN-1995; 95US-0477944.
 XX (DAND) DNA FABRIC CANCER INST INC.
 XX (HBR) REPLICATION CORE.
 PP Freeman GJ, Gray GS, Nadler LM;
 PI WPI; 1997-077669/07.
 DA N-PEB3; ART49182.
 DR DNA encoding A B7-2 fusion protein - used to enhance or down
 PT regulate B lymphocyte antigens
 XX Example 6; Page 102-103; 71pp; English.
 CC Mouse B-lymphocyte antigen B7-2 (AA080468) is a CTLA4/CD28 ligand
 CC and its amino acid sequence was deduced from the cDNA sequence
 CC line library. Novel fusion proteins comprising the extracellular
 CC region, variable region-like or constant region-like domains of
 CC heavy chain constant region can be expressed in host cells and used
 CC to enhance or suppress T cell-mediated immune responses.
 XX Sequence 369 AA;

Query Match 100.0%; Score 1599; DB 18; Length 309;
 Best Local Similarity 100.0%; Pred. No. 12-17;
 Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDPRCTGIALIFVTVALISDAVSFTQVFNPTALPCPTTAQNISELVFPQD 60
 DB 1 MDPRCTGIALIFVTVALISDAVSFTQVFNPTALPCPTTAQNISELVFPQD 60
 QY 61 QKLVYENIATGTELSVNAKYLGRTSFDNRMTLRANVOIKMGSDCFQKPPFS 120
 DB 61 QKLVYENIATGTELSVNAKYLGRTSFDNRMTLRANVOIKMGSDCFQKPPFS 120
 QY 121 ILLOQTLETSVIAVFSEPEIKLAQVNTGNIILNVQIKSGQPKPKPWFLITNSTEY 180
 DB 121 ILLOQTLETSVIAVFSEPEIKLAQVNTGNIILNVQIKSGQPKPKPWFLITNSTEY 180
 QY 181 GNNQVIGDNVTELSISGLSFFDQVMMHTVVCVLTETSMKISKSPINFTQEPFQ 240
 DB 181 GNNQVIGDNVTELSISGLSFFDQVMMHTVVCVLTETSMKISKSPINFTQEPFQ 240
 QY 241 TWKETSATVALLVWMLLIIVCHKPKQPSRNTASKLRSDMADRTINKLELQ 300
 DB 241 TWKETSATVALLVWMLLIIVCHKPKQPSRNTASKLRSDMADRTINKLELQ 300
 QY 301 IASAPNAE 309
 DB 301 IASAPNAE 309
 RESULT 2
 AA077639
 XX AA077639 standard; Protein; 309 AA.
 AC AA077639;
 XX 19-MAR-1999 (first entry)
 DT
 XX

DE Mouse B7-2 antigen.
 XX B7-2 antigen; mammalian tumour cell; T cell costimulation; CD28 ligand;
 XX CTLA4 ligand; Therapy; T-cell response; mouse.
 CS Mus sp.
 XX US864110-A.
 XX 19-JAN-1999.
 PP 10-MAY-1995; 95US-0456104.
 XX 10-MAY-1995; 95US-0456104.
 PP 03-NOV-1993; 93US-0147773.
 XX (DAND) DNA FABRIC CANCER INST INC.
 XX Freeman GJ, Gray GS, Nadler LM;
 PI WPI; 1997-030349/11.
 DA N-PEB3; AA050786.
 DR Tumour cell transfected to express B7-2 molecule - useful for tumour
 PT therapy by stimulating T-cell response
 XX Discharge; Column 31-34; 27pp; English.
 CC This sequence is the mouse B7-2 antigen, which can be used in the
 CC method of the invention. The method is for transfecting an isolated
 CC mammalian tumour cell with an exogenous nucleic acid molecule encoding a
 CC B7-2 antigen. The isolated mammalian tumour cell is capable of the
 CC binding a CD28 or CTLA4 ligand. The method is useful for treating tumours
 CC by stimulating a T-cell response against tumour cells in vivo.
 XX Sequence 309 AA;

Query Match 100.0%; Score 1599; DB 20; Length 309;
 Best Local Similarity 100.0%; Pred. No. 12-17;
 Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDPRCTGIALIFVTVALISDAVSFTQVFNPTALPCPTTAQNISELVFPQD 60
 DB 1 MDPRCTGIALIFVTVALISDAVSFTQVFNPTALPCPTTAQNISELVFPQD 60
 QY 61 QKLVYENIATGTELSVNAKYLGRTSFDNRMTLRANVOIKMGSDCFQKPPFS 120
 DB 61 QKLVYENIATGTELSVNAKYLGRTSFDNRMTLRANVOIKMGSDCFQKPPFS 120
 QY 121 ILLOQTLETSVIAVFSEPEIKLAQVNTGNIILNVQIKSGQPKPKPWFLITNSTEY 180
 DB 121 ILLOQTLETSVIAVFSEPEIKLAQVNTGNIILNVQIKSGQPKPKPWFLITNSTEY 180
 QY 181 GNNQVIGDNVTELSISGLSFFDQVMMHTVVCVLTETSMKISKSPINFTQEPFQ 240
 DB 181 GNNQVIGDNVTELSISGLSFFDQVMMHTVVCVLTETSMKISKSPINFTQEPFQ 240
 QY 241 TWKETSATVALLVWMLLIIVCHKPKQPSRNTASKLRSDMADRTINKLELQ 300
 DB 241 TWKETSATVALLVWMLLIIVCHKPKQPSRNTASKLRSDMADRTINKLELQ 300
 QY 301 IASAPNAE 309
 DB 301 IASAPNAE 309
 RESULT 3
 AA077639
 XX AA077639 standard; Protein; 309 AA.
 AC AA077639;
 XX 19-MAR-1999 (first entry)
 DT
 XX

Matches 158; Conservative 45; Mismatches 91; Indels 13; Gaps 5;

QY 1 MDPQCTNGALILPTVLLISNSVETQYFNGTATLPCTFMKQNSISELWFMQDQ 60
 DB 1 MDPQCTNGALILPTVLLISNSVETQYFNGTATLPCTFMKQNSISELWFMQDQ 60
 QY 61 OKLVLAVETVLAKEPDSVNSKYGRTSISDSTPLRANJQIMOKGLVQCIINHKAFOM 120
 DB 61 OKLVLAVETVLAKEPDSVNSKYGRTSISDSTPLRANJQIMOKGLVQCIINHKAFOM 120
 QY 121 ILIQGLTVELVANSFPEIKLAQNVGSGNLTCSQGPQKPKVAVL---TNSIN 178
 DB 121 ILIQGLTVELVANSFPEIKLAQNVGSGNLTCSQGPQKPKVAVL---TNSIN 178
 QY 179 EYGNQNSQNTVELTSSNISLSFDFQWVTVVVLTEEMISKQNLFTQEPFS 238
 DB 179 EYGNQNSQNTVELTSSNISLSFDFQWVTVVVLTEEMISKQNLFTQEPFS 238
 QY 239 P---OTTWMEITASVALLNL---LIVCHKPKQSP---SNTASKLERSDNAUR 289
 DB 239 P---OTTWMEITASVALLNL---LIVCHKPKQSP---SNTASKLERSDNAUR 289
 QY 290 ETILAKR 296
 DB 290 ETILAKR 296
 QY 295 EKHIPE 305
 DB 295 EKHIPE 305

RESULT 11

AM73638
 D AA73638 standard; Protein, 329 AA.
 AC AA73638;
 AC AA73638;
 AC 23-MAR-1999 (first entry)
 AC Human B7-2 antigen.

XX B7-2 antigen; mammalian tumour cell, T cell costimulation, CD28 ligand.
 XX CTLA4 ligand; therapy; T-cell response; human.

XX Homo sapiens.

XX US566110-A.

XX 19-JAN-1999.

XX 30-MAY-1995; 95US-0456104.

XX 30-MAY-1995; 95US-0456104.

XX 03-NOV-1993; 93US-0147773.

XX (DND) DANA FARBER CANCER INST INC.

XX Freeman GJ, Gray GS, Nadler LM;

XX NFI; 1995-130194/11.

XX N-PSDB; AA055784.

XX Tumor cell transfected to express B7-2 molecule - useful for tumour

XX therapy by stimulating T-cell response

XX Claim 10; Column 27-30; 27pp; English.

XX This sequence is the human B7-2 antigen, which can be used in the

XX mammalian tumour cell with an exogenous nucleic acid encoding a

XX mammalian B7-2 molecule, where the B7-2 molecule is expressed in the

XX T cell response. Consistent with the invention, a cell and is capable of

XX binding a CD28 or CTLA4 ligand, and is useful for stimulating tumours

XX by stimulating a T-cell response against tumour cells in vivo.

XX Sequence 329 AA;

Query Match 45-58; Score 743.5; DB 20; Length 329;
 Best Local Similarity 57.5%;
 Matches 158; Conservative 45; Mismatches 91; Indels 13; Gaps 5;

QY 1 MDPQCTNGALILPTVLLISNSVETQYFNGTATLPCTFMKQNSISELWFMQDQ 60
 DB 1 MDPQCTNGALILPTVLLISNSVETQYFNGTATLPCTFMKQNSISELWFMQDQ 60
 QY 61 OKLVLAVETVLAKEPDSVNSKYGRTSISDSTPLRANJQIMOKGLVQCIINHKAFOM 120
 DB 61 OKLVLAVETVLAKEPDSVNSKYGRTSISDSTPLRANJQIMOKGLVQCIINHKAFOM 120
 QY 121 ILIQGLTVELVANSFPEIKLAQNVGSGNLTCSQGPQKPKVAVL---TNSIN 178
 DB 121 ILIQGLTVELVANSFPEIKLAQNVGSGNLTCSQGPQKPKVAVL---TNSIN 178
 QY 179 EYGNQNSQNTVELTSSNISLSFDFQWVTVVVLTEEMISKQNLFTQEPFS 238
 DB 179 EYGNQNSQNTVELTSSNISLSFDFQWVTVVVLTEEMISKQNLFTQEPFS 238
 QY 239 P---OTTWMEITASVALLNL---LIVCHKPKQSP---SNTASKLERSDNAUR 289
 DB 239 P---OTTWMEITASVALLNL---LIVCHKPKQSP---SNTASKLERSDNAUR 289
 QY 290 ETILAKR 296
 DB 290 ETILAKR 296
 QY 295 EKHIPE 305
 DB 295 EKHIPE 305

RESULT 12

AA837085
 D AA837085 standard; Protein, 329 AA.
 AC AA837085;
 AC AA837085;
 AC 28-MAR-2001 (first entry)

XX Human B lymphocyte antigen B7-2 from clone 29.

XX Immunomodulator; fusion protein; human; murine; mouse; lymphocyte; CD28;

XX antigen; extracellular domain; CTLA4; immunoglobulin constant region;

XX T cell-mediated immune response, transplacental; vaccination.

XX Homo sapiens.

XX US613016-A.

XX 10-OCT-2000.

XX 26-JUL-1994; 94US-0280757.

XX 26-JUL-1994; 94US-0280757.

XX 19-AUG-1993; 93US-0101624.

XX 19-AUG-1993; 93US-0101624.

XX 03-NOV-1993; 93US-0147773.

XX (DND) DANA FARBER CANCER INST INC.

XX (REPK) REPLICON CORP.

XX Freeman GJ, Nadler LM, Gray GS, Greenfield E;

XX NFI; 2000-056602/63.

XX N-PSDB; AA055784.

XX Nucleic acid and fusion proteins of CTLA4/CD28 ligands, useful for

XX immunomodulation, especially in the treatment of cancer, especially

XX during tissue, skin or organ transplantation, or in graft-versus-host

XX disease.

XX Claim 23; Fig 8; 8pp; English.

XX The invention relates to an isolated nucleic acid molecule encoding a

XX protein comprising a first nucleotide sequence encoding a first


```

SQ Sequence 323 AA, 444; Score 710.5; DB 16; Length 323;
Query Match Similarity: 84; Percent Identical: 51;
Matches 153; Conservative 44; Mismatches 91; Indels 13; Gaps 5;

Oy 7 MGAALIFVYLLISDAVSVEIATNCTVYLCPTKAAQNSISLSVPTWQOQKLVY 66
Db 1 MGLSNILFWAFLEGAFLQIAVFNETALPCFANSONGLSLVPTWQOENLVN 60
Oy 67 EKVGLTELSQANVYLCRETFQANWTLALANVQYEMQSVCTCKEPTGSILOOT 126
Db 61 EYVLGKEFDSVNSKWTCTSPDSQWTLALNLAITXGLQYCIHHKAPTONIRHQW 120
Oy 127 LTELVSINAPSPETKLAQWVTGNSGINTACTSKQCHPKQNVYLI--TNSINVEYDGM 184
Db 121 NSLSVLNAPSQPEIUPSINITENVYINLTCSSIHQPEPKNSVILRTKNTIETGIM 180
Oy 185 QISQDNVTELSINSLSPFDQVHMTVCVLETESMKISSKELNFTQEPREP--QT 241
Db 181 OKSQDNVTELSISLVSPFDQVHMTVCVLETESMKISSKELNFTQEPREP--QT 241
Oy 242 YHEITATVYALLNW--LIVCHKEPQPSRP---SNTASKLERISNADRETINLK 295
Db 241 PW--LIVCHKEPQPSRP---SNTASKLERISNADRETINLK 295
Oy 296 E 296
Db 299 E 299

```

Search completed, February 13, 2003, 11:30:59
 Job time : 31.4496 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model.

Run On: February 13, 2003, 11:32:49, Search time 16.9514 Seconds
(Without alignments)
465.720 Million cell updates/sec

US-09-425-516-23

Title: 1599
Perfect score: 1.000
Sequence: 1 KSPYKWEIAILVTVLL.....ETIKLEPFAQNAE 309

Scoring table: BLOSUM62
Gap: 10.0, Gapex: 0.5

Searched: 140259 seqs, 35548876 residues

Total number of hits satisfying chosen parameters: 140259

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Databases :

Published Applications AA*
1: /cgn2_6/prodata2/pubaa/us06_NEM_PUB pep.*
2: /cgn2_6/prodata2/pubaa/us06_NEM_PUB pep.*
3: /cgn2_6/prodata2/pubaa/us06_NEM_PUB pep.*
4: /cgn2_6/prodata2/pubaa/us06_PUBCOW pep.*
5: /cgn2_6/prodata2/pubaa/us06_PUBCOW pep.*
6: /cgn2_6/prodata2/pubaa/us07_PUBCOW pep.*
7: /cgn2_6/prodata2/pubaa/PTTIS_PUBCOW pep.*
8: /cgn2_6/prodata2/pubaa/US03_PUBCOW pep.*
9: /cgn2_6/prodata2/pubaa/US05_NEM_PUB pep.*
10: /cgn2_6/prodata2/pubaa/US05_PUBCOW pep.*
11: /cgn2_6/prodata2/pubaa/US06_PUBCOW pep.*
12: /cgn2_6/prodata2/pubaa/US06_PUBCOW pep.*
13: /cgn2_6/prodata2/pubaa/US06_NEM_PUB pep.*
14: /cgn2_6/prodata2/pubaa/US06_PUBCOW pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	1599	100.0	309	9 US-09-441-411-13	Sequence 13, Appl
2	1599	100.0	309	9 US-09-441-411-18	Sequence 18, Appl
3	1599	100.0	309	9 US-09-441-411-24	Sequence 24, Appl
4	1599	100.0	309	10 US-09-837-867A-21	Sequence 21, Appl
5	1596	98.6	314	9 US-09-441-411-19	Sequence 19, Appl
6	1576	98.6	314	9 US-09-441-411-13	Sequence 13, Appl
7	1576	98.6	314	10 US-09-837-867A-13	Sequence 13, Appl
8	1567	98.0	356	9 US-09-441-411-12	Sequence 12, Appl
9	1567	98.0	356	9 US-09-441-411-16	Sequence 16, Appl
10	1567	98.0	356	9 US-09-441-411-17	Sequence 17, Appl
11	1567	98.0	356	9 US-09-441-411-20	Sequence 20, Appl
12	1562	97.7	303	9 US-09-441-411-20	Sequence 20, Appl
13	743.5	46.5	339	8 US-08-592-11-4	Sequence 4, Appl
14	743.5	46.5	339	8 US-08-592-11-4	Sequence 4, Appl
15	743.5	46.5	339	10 US-09-837-867A-23	Sequence 23, Appl
16	743.5	46.5	339	9 US-09-837-867A-23	Sequence 23, Appl
17	710.5	44.4	323	9 US-09-896-738-11	Sequence 11, Appl
18	710.5	44.4	323	9 US-09-896-738-11	Sequence 11, Appl
19	710.5	44.4	323	9 US-09-441-411-22	Sequence 22, Appl

20	710.5	44.4	323	10 US-09-955-866-5	Sequence 5, Appl
21	710	44.4	324	10 US-09-910-174A-6	Sequence 6, Appl
22	707	44.2	320	10 US-09-842-899A-5	Sequence 5, Appl
23	707	44.2	320	10 US-09-842-899A-5	Sequence 5, Appl
24	640.5	40.1	329	10 US-09-103-510-6	Sequence 6, Appl
25	640.5	40.1	329	10 US-09-103-510-6	Sequence 6, Appl
26	630	40.1	329	10 US-09-103-510-6	Sequence 6, Appl
27	630	40.1	329	10 US-09-103-510-6	Sequence 6, Appl
28	227.5	14.2	306	10 US-09-837-867A-70	Sequence 10, Appl
29	215.5	13.5	305	10 US-09-910-174A-28	Sequence 28, Appl
30	215.5	13.5	305	10 US-09-910-174A-28	Sequence 28, Appl
31	182	11.4	303	9 US-09-896-738-13	Sequence 13, Appl
32	182	11.4	302	9 US-09-915-789A-18	Sequence 18, Appl
33	182	11.4	302	10 US-09-915-789A-18	Sequence 18, Appl
34	182	11.4	302	10 US-09-955-866-7	Sequence 7, Appl
35	182	11.4	309	10 US-09-910-174A-7	Sequence 7, Appl
36	182	11.4	316	10 US-09-910-174A-7	Sequence 7, Appl
37	182	11.4	316	10 US-09-910-174A-7	Sequence 7, Appl
38	182	11.4	344	10 US-09-764-853-610	Sequence 610, Appl
39	182	11.4	344	10 US-09-764-853-610	Sequence 610, Appl
40	182	11.4	345	10 US-09-764-853-810	Sequence 810, Appl
41	182	11.4	345	10 US-09-764-853-810	Sequence 810, Appl
42	181	11.3	316	9 US-09-780-632-4	Sequence 4, Appl
43	181	11.3	316	9 US-09-780-632-4	Sequence 4, Appl
44	181	11.3	316	10 US-09-789-561-135	Sequence 135, Appl
45	180	11.3	316	10 US-09-789-561-135	Sequence 135, Appl
46	180	11.3	316	9 US-09-896-738-14	Sequence 14, Appl
47	180	11.3	316	9 US-09-896-738-14	Sequence 14, Appl
48	180	11.3	316	9 US-09-978-697-137	Sequence 137, Appl
49	180	11.3	316	9 US-09-978-697-137	Sequence 137, Appl

ALIGNMENTS

RESULT 1
US-09-441-411-13
; Sequence 13, Application US/09/441411
; US-09-441-411-13
; GENERAL INFORMATION: US/09/441411
; APPLICANT: Scholler, Nathalie B.
; APPLICANT: Scholler, Nathalie B.
; APPLICANT: Scholler, Nathalie B.
; APPLICANT: Helistrom, Ingemar
; APPLICANT: Helistrom, Ingemar
; TITLE REFERENCE: US/09/31409
; CURRENT APPLICATION NUMBER: US/09/441-411
; CURRENT FILING DATE: 1999-11-16
; SOFTWARE: FASTSD for Windows Version 4.0
; SEQ ID NO 13
; SEQ ID NO 13
; TYPE: BPT
; ORGANISM: Mus musculus
US-09-441-411-13

Query Match	100.0%	Score 1599;	DB 9;	Length 309;
Best Local Similarity	100.0%	Pred. No. 5,7e-119;		
Matches 309;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MDPCMGALIFVTVLLISDINVSQVFNVAIVNIACTFPAQKISLSGLVFPQD	60	
Db	1	MDPCMGALIFVTVLLISDINVSQVFNVAIVNIACTFPAQKISLSGLVFPQD	60	
Qy	61	QULVTEHTLEKUSLVNATLGFSTSDNNMTLRUNVQIKMGSTCFCKPPTGS	120	
Db	61	QULVTEHTLEKUSLVNATLGFSTSDNNMTLRUNVQIKMGSTCFCKPPTGS	120	
Qy	121	LIHQETFEVYSEFSEKVAQVYKQNSVSTTSGQSGPQKQWFLINSTNEY	180	
Db	121	LIHQETFEVYSEFSEKVAQVYKQNSVSTTSGQSGPQKQWFLINSTNEY	180	
Qy	181	QDMQISQDNTVFLSINLSISFPDQWHVTVVLFETSMKISLKFNTQFSPQ	240	
Db	181	QDMQISQDNTVFLSINLSISFPDQWHVTVVLFETSMKISLKFNTQFSPQ	240	
Qy	241	TYWKEITASYVALLVLLVILQVUKPQSPSPENTAKJFSDNADINKELEPQ	300	

```

; SEQ ID NO 24
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-441-411-24
Query Match
  Local Similarity 100.0%; Score 1599; DB 9; Length 309;
  Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2
US-09-441-411-18
; Application US/09/441-411
; Publication No US2003008342A1
; GENERAL INFORMATION:
; APPLICANT: Scholer, Nathalie B.
; APPLICANT: Dussier, Mary Ingegrid
; APPLICANT: Helletrom, Ingegrid
; APPLICANT: Helletrom, Karl Erik
; FILE REFERENCE: 720033 409 ACCEPTOR ANTIGEN VACCINES
; CURRENT APPLICATION NUMBER: US/09/441-411
; PRIOR FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-441-411-19
Query Match
  Local Similarity 100.0%; Score 1599; DB 9; Length 309;
  Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MDPCTMGALLIFVTLLISDAVSVEYATFNCTATPCPTKAQNSISELWVMDQ 60
Db 1 MDPCTMGALLIFVTLLISDAVSVEYATFNCTATPCPTKAQNSISELWVMDQ 60
Oy 61 OKULVENVLTGKDSANVYKLTGTSFERNMTLJAHVQIKMSGYCTCKPKPTSS 120
Db 61 OKULVENVLTGKDSANVYKLTGTSFERNMTLJAHVQIKMSGYCTCKPKPTSS 120
Oy 121 ILLOOTTELSVTFANFSEPEIKLAQVYNGSINLCTSKQGHKPKWFLTNSTNEY 180
Db 121 ILLOOTTELSVTFANFSEPEIKLAQVYNGSINLCTSKQGHKPKWFLTNSTNEY 180
Oy 181 GGNQVLSQNVTELSISNLSLSPFGDVMHTVVCVLETSKISKPINFQPPSPQ 240
Db 181 GGNQVLSQNVTELSISNLSLSPFGDVMHTVVCVLETSKISKPINFQPPSPQ 240
Oy 241 TWKEITASTVALLVMALLIVCHKGNPSPSTASKERSADRETNKLEPQ 300
Db 241 TWKEITASTVALLVMALLIVCHKGNPSPSTASKERSADRETNKLEPQ 300
Oy 301 ISAKPNAE 309
Db 301 ISAKPNAE 309

```

```

RESULT 4
US-09-837-867A-21
; Application US/09/837867A
; Sequence 21
; Publication No US20030424A1
; GENERAL INFORMATION:
; APPLICANT: Shape, Ariens H.
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; APPLICANT: Scapellato, Joseph
; FILE REFERENCE: 8M-120FADV
; TITLE OF INVENTION: Nucleolus and T Cell Costimulatory
; CURRENT APPLICATION NUMBER: US/09/837, 867A
; PRIOR FILING DATE: 1994-03-02
; PRIOR APPLICATION NUMBER: 08/205,697
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-837-867A-21
Query Match
  Local Similarity 100.0%; Score 1599; DB 10; Length 309;
  Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MDPCTMGALLIFVTLLISDAVSVEYATFNCTATPCPTKAQNSISELWVMDQ 60
Db 1 MDPCTMGALLIFVTLLISDAVSVEYATFNCTATPCPTKAQNSISELWVMDQ 60
Oy 61 OKULVENVLTGKDSANVYKLTGTSFERNMTLJAHVQIKMSGYCTCKPKPTSS 120
Db 61 OKULVENVLTGKDSANVYKLTGTSFERNMTLJAHVQIKMSGYCTCKPKPTSS 120
Oy 121 ILLOOTTELSVTFANFSEPEIKLAQVYNGSINLCTSKQGHKPKWFLTNSTNEY 180
Db 121 ILLOOTTELSVTFANFSEPEIKLAQVYNGSINLCTSKQGHKPKWFLTNSTNEY 180

```

Db 121 ILLOQTTELSTJANFBEPEKLAQVNGSINLTCKQPKPKWVLNSTNEY 180
 Oy 181 QNNQOQVQVPEFSISNSLSFPGQVMMTVVLTSTKSNLSJPLFTPEPQ 240
 ; FILE REFERENCE: 730031.409 US/09/441.411
 ; APPLICANT: Hellstrom, Karl Erik
 ; TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
 ; CURRENT FILING DATE: 1994-11-16
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: FastsEQ for Windows Version 4.0
 ; LENGTH: 314
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 Db 301 INAKPMAR 309
 Db 301 INAKPMAR 309

RESULT 5
 ; Sequence 14, Application US/0941411
 ; Publication No. US20030008342A1
 ; APPLICANT: Scholler, Nathalie B.
 ; APPLICANT: Diehl, Mary L.
 ; APPLICANT: Hellstrom, Inggerd
 ; TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
 ; FILE REFERENCE: 730031.409 US/09/441.411
 ; CURRENT FILING DATE: 1994-11-16
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: FastsEQ for Windows Version 4.0
 ; LENGTH: 314
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 Us-09-441-411-14

Query Match 98.64, Score 1576; Db 9; Length 314;
 Best Local Similarity 100.00; Pseq 3.8e-117;
 Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 CTGCAALIFVTVLLISDANSVTOAFNGTALPCPTCAQNSISELVPMQOQKLV 64
 Db 10 CTGCAALIFVTVLLISDANSVTOAFNGTALPCPTCAQNSISELVPMQOQKLV 69
 Oy 65 LYRHLTEKLGDNVAKLTGTFRRNMVTLHNVQIKOMSVYDCTQKPEPTGIILO 124
 Db 70 LYRHLTEKLGDNVAKLTGTFRRNMVTLHNVQIKOMSVYDCTQKPEPTGIILO 129
 Oy 125 OTTELSTJANFBEPEKLAQVNGSINLTCKQPKPKWVLNSTNEYDGM 184
 Db 130 OTTELSTJANFBEPEKLAQVNGSINLTCKQPKPKWVLNSTNEYDGM 189
 Oy 185 QIQQNVTEFLSISNSLSFPGQVMMTVVLTSTKSNLSJPLFTPEPQPYWK 244
 Db 190 QIQQNVTEFLSISNSLSFPGQVMMTVVLTSTKSNLSJPLFTPEPQPYWK 249
 Oy 245 EITATVALLVLLIVCHKQPKQSPSTASKERSDAGRETINLKEPQIAGA 304
 Db 250 EITATVALLVLLIVCHKQPKQSPSTASKERSDAGRETINLKEPQIAGA 309
 Oy 305 KPMAR 309
 Db 310 KPMAR 314

RESULT 6
 ; Sequence 19, Application US/0944141
 ; Publication No. US20030008342A1
 ; APPLICANT: Scholler, Nathalie B.
 ; APPLICANT: Hellstrom, Inggerd

; APPLICANT: Hellstrom, Karl Erik
 ; TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
 ; FILE REFERENCE: 730031.409 US/09/441.411
 ; CURRENT FILING DATE: 1994-11-16
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: FastsEQ for Windows Version 4.0
 ; LENGTH: 314
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 Us-09-441-411-19

Query Match 98.64, Score 1576; Db 9; Length 314;
 Best Local Similarity 100.00; Pseq 3.8e-117;
 Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 CTGCAALIFVTVLLISDANSVTOAFNGTALPCPTCAQNSISELVPMQOQKLV 64
 Db 10 CTGCAALIFVTVLLISDANSVTOAFNGTALPCPTCAQNSISELVPMQOQKLV 69
 Oy 65 LYRHLTEKLGDNVAKLTGTFRRNMVTLHNVQIKOMSVYDCTQKPEPTGIILO 124
 Db 70 LYRHLTEKLGDNVAKLTGTFRRNMVTLHNVQIKOMSVYDCTQKPEPTGIILO 129
 Oy 125 OTTELSTJANFBEPEKLAQVNGSINLTCKQPKPKWVLNSTNEYDGM 184
 Db 130 OTTELSTJANFBEPEKLAQVNGSINLTCKQPKPKWVLNSTNEYDGM 189
 Oy 185 QIQQNVTEFLSISNSLSFPGQVMMTVVLTSTKSNLSJPLFTPEPQPYWK 244
 Db 190 QIQQNVTEFLSISNSLSFPGQVMMTVVLTSTKSNLSJPLFTPEPQPYWK 249
 Oy 245 EITATVALLVLLIVCHKQPKQSPSTASKERSDAGRETINLKEPQIAGA 304
 Db 250 EITATVALLVLLIVCHKQPKQSPSTASKERSDAGRETINLKEPQIAGA 309
 Oy 305 KPMAR 309
 Db 310 KPMAR 314

RESULT 7
 ; Sequence 13, Application US/0983767A
 ; Publication No. US20020086431A1
 ; APPLICANT: Sharpe, Aylene H.
 ; APPLICANT: Lee, M.
 ; APPLICANT: Freeman, Gordon J.
 ; APPLICANT: Nadler, Lee M.
 ; TITLE OF INVENTION: Molecular and Uses Thereof
 ; FILE REFERENCE: BNI-130CPNV
 ; CURRENT APPLICATION NUMBER: US/09/837,867A
 ; PRIOR FILING DATE: 1994-03-02
 ; NUMBER OF SEQ ID NOS: 1
 ; SOFTWARE: FastsEQ for Windows Version 4.0
 ; LENGTH: 314
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 Us-09-837-867A-13

Query Match 98.64, Score 1576; Db 10; Length 314;
 Best Local Similarity 100.00; Pseq 3.8e-117;
 Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 CTGCAALIFVTVLLISDANSVTOAFNGTALPCPTCAQNSISELVPMQOQKLV 64
 Db 10 CTGCAALIFVTVLLISDANSVTOAFNGTALPCPTCAQNSISELVPMQOQKLV 69

```

Qy 65 LVHYHGTGKLSVNAKYLGRTSFDNNWFLRLHNVQIKMGVSDFCKQKPGTSSILQ 124
Db 70 QYHGTGKLSVNAKYLGRTSFDNNWFLRLHNVQIKMGVSDFCKQKPGTSSILQ 129
Qy 125 QYHGTGKLSVNAKYLGRTSFDNNWFLRLHNVQIKMGVSDFCKQKPGTSSILQ 184
Db 130 QYHGTGKLSVNAKYLGRTSFDNNWFLRLHNVQIKMGVSDFCKQKPGTSSILQ 189
Qy 185 QYHGTGKLSVNAKYLGRTSFDNNWFLRLHNVQIKMGVSDFCKQKPGTSSILQ 244
Db 190 QYHGTGKLSVNAKYLGRTSFDNNWFLRLHNVQIKMGVSDFCKQKPGTSSILQ 249
Qy 245 QYHGTGKLSVNAKYLGRTSFDNNWFLRLHNVQIKMGVSDFCKQKPGTSSILQ 304
Db 250 QYHGTGKLSVNAKYLGRTSFDNNWFLRLHNVQIKMGVSDFCKQKPGTSSILQ 309
Qy 305 KPAHE 309
Db 310 KPAHE 314

RESULT 8
US-09-441-411-11
; Publication No. US20030083421
; GENERAL INFORMATION: Nathalie B.
; APPLICANT: Disle, Mary L., Ingegerd
; APPLICANT: Hallstrom, Karl Erik
; FILE REFERENCE: 710033.409
; CURRENT APPLICATION NUMBER: US/09/441.411
; FILING DATE: 1995-11-16
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 356
; ORGANISM: Nus musculus
; TYPE: PRT
Query Match 98.0%; Score 1567; DB 9; Length 356;
Local Similarity 100.0%; Pred. No. 2,3e+16;
Matches 304; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TWGALILFTVLLISDAVSTQVFNATYVLPCTFAKNISLSLSEVFWQDQGLVL 65
Db 53 TWGALILFTVLLISDAVSTQVFNATYVLPCTFAKNISLSLSEVFWQDQGLVL 112
Qy 66 VEHVUHTGKLSVNAKYLGRTSFDNNWFLRLHNVQIKMGVSDFCKQKPGTSSILQ 125
Db 113 VEHVUHTGKLSVNAKYLGRTSFDNNWFLRLHNVQIKMGVSDFCKQKPGTSSILQ 172
Qy 126 TITELSVINAFSEELKLAQVNGSGILCTCKQKPEKPKMYFLINSTEYGNQ 185
Db 173 TITELSVINAFSEELKLAQVNGSGILCTCKQKPEKPKMYFLINSTEYGNQ 232
Qy 186 ISQDNTVLEFSINLSLSFDPQVWHYVCTVLETSKISKLNADRETINKELEPOLASAK 245
Db 233 ISQDNTVLEFSINLSLSFDPQVWHYVCTVLETSKISKLNADRETINKELEPOLASAK 292
Qy 246 ITASVYVALLVLLIIVCHKKNQSPRENTAKSLERSDNADRETINKELEPOLASAK 305
Db 293 ITASVYVALLVLLIIVCHKKNQSPRENTAKSLERSDNADRETINKELEPOLASAK 352
Qy 306 PNAE 309
Db 353 PNAE 356

RESULT 9
US-09-441-411-11
; Publication No. US20030083421
; GENERAL INFORMATION: Nathalie B.
; APPLICANT: Disle, Mary L., Ingegerd
; APPLICANT: Hallstrom, Karl Erik
; FILE REFERENCE: 710033.409
; CURRENT APPLICATION NUMBER: US/09/441.411
; FILING DATE: 1995-11-16
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 356
; ORGANISM: Nus musculus
; TYPE: PRT
Query Match 98.0%; Score 1567; DB 9; Length 356;
Local Similarity 100.0%; Pred. No. 2,3e+16;
Matches 304; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

US-09-441-411-12
; Publication No. US20030083421
; GENERAL INFORMATION: Nathalie B.
; APPLICANT: Disle, Mary L., Ingegerd
; APPLICANT: Hallstrom, Karl Erik
; FILE REFERENCE: 710033.409
; CURRENT APPLICATION NUMBER: US/09/441.411
; FILING DATE: 1995-11-16
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 356
; ORGANISM: Nus musculus
; TYPE: PRT
Query Match 98.0%; Score 1567; DB 9; Length 356;
Local Similarity 100.0%; Pred. No. 2,3e+16;
Matches 304; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TWGALILFTVLLISDAVSTQVFNATYVLPCTFAKNISLSLSEVFWQDQGLVL 65
Db 53 TWGALILFTVLLISDAVSTQVFNATYVLPCTFAKNISLSLSEVFWQDQGLVL 112
Qy 66 VEHVUHTGKLSVNAKYLGRTSFDNNWFLRLHNVQIKMGVSDFCKQKPGTSSILQ 125
Db 113 VEHVUHTGKLSVNAKYLGRTSFDNNWFLRLHNVQIKMGVSDFCKQKPGTSSILQ 172
Qy 126 TITELSVINAFSEELKLAQVNGSGILCTCKQKPEKPKMYFLINSTEYGNQ 185
Db 173 TITELSVINAFSEELKLAQVNGSGILCTCKQKPEKPKMYFLINSTEYGNQ 232
Qy 186 ISQDNTVLEFSINLSLSFDPQVWHYVCTVLETSKISKLNADRETINKELEPOLASAK 245
Db 233 ISQDNTVLEFSINLSLSFDPQVWHYVCTVLETSKISKLNADRETINKELEPOLASAK 292
Qy 246 ITASVYVALLVLLIIVCHKKNQSPRENTAKSLERSDNADRETINKELEPOLASAK 305
Db 293 ITASVYVALLVLLIIVCHKKNQSPRENTAKSLERSDNADRETINKELEPOLASAK 352
Qy 306 PNAE 309
Db 353 PNAE 356

RESULT 10
US-09-441-411-16
; Publication No. US20030083421
; GENERAL INFORMATION: Nathalie B.
; APPLICANT: Disle, Mary L., Ingegerd
; APPLICANT: Hallstrom, Karl Erik
; FILE REFERENCE: 710033.409
; CURRENT APPLICATION NUMBER: US/09/441.411
; FILING DATE: 1995-11-16
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 356
; ORGANISM: Nus musculus
; TYPE: PRT
Query Match 98.0%; Score 1567; DB 9; Length 356;
Local Similarity 100.0%; Pred. No. 2,3e+16;
Matches 304; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```


Oy 6 TNGALHIFVTLISDAVETQVNTGYATFCPTQAQNIISLSLWVPMQOQKLV 65
 53 TNGALHIFVTLISDAVETQVNTGYATFCPTQAQNIISLSLWVPMQOQKLV 112
 Oy 66 YEHVUTKELDSWAKYLGRTSFDRNNWTLRLHNVQIKDMSYDCTOKKPTGSIHQ 125
 Db 113 YEHVUTKELDSWAKYLGRTSFDRNNWTLRLHNVQIKDMSYDCTOKKPTGSIHQ 172
 Oy 126 TLTLSYVIANFSEPEIKLAQNTGSGNLCTSKQKPPKPMFLINSTEINVDNM 185
 Db 173 TLTLSYVIANFSEPEIKLAQNTGSGNLCTSKQKPPKPMFLINSTEINVDNM 232
 Oy 186 ISQDWTLEFSINSLSPFQPMWMTVCULSTSKSPKPLFTQFSPOTWKE 245
 Db 245 ISQDWTLEFSINSLSPFQPMWMTVCULSTSKSPKPLFTQFSPOTWKE 292
 Oy 246 ITASTVALLWMLLIIVCHKQKPPQSPSTASKLRSNADRETINKLEFQIASK 305
 Db 293 ITASTVALLWMLLIIVCHKQKPPQSPSTASKLRSNADRETINKLEFQIASK 352
 Oy 306 PNAE 309
 Oy 352 PNAE 356

RESULT 11
 US-09-441-411-17
 ; Sequence 17, Application US/0941411
 ; Publication No. US2003008342A1
 ; APPLICANT: Scholler, Nathalie B.
 ; APPLICANT: Disis, Mary L.
 ; APPLICANT: Helstrom, Ingegerd
 ; APPLICANT: Helstrom, Karl Erik
 ; TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
 ; FILE REFERENCE: 730033.409 US/09/441.411
 ; CURRENT FILING DATE: 1999-11-16
 ; NUMBER OF SEQ ID NOS: 26
 ; SEQ ID NO 15
 ; SOFTWARE: PatsEQ for Windows Version 4.0
 ; LENGTH: 356
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-09-441-411-17

Query Match
 Best Local Similarity 100.0%; Seed No. 2,34-16; Length 356;
 Matches 304; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 6 TNGALHIFVTLISDAVETQVNTGYATFCPTQAQNIISLSLWVPMQOQKLV 65
 Db 53 TNGALHIFVTLISDAVETQVNTGYATFCPTQAQNIISLSLWVPMQOQKLV 112
 Oy 66 YEHVUTKELDSWAKYLGRTSFDRNNWTLRLHNVQIKDMSYDCTOKKPTGSIHQ 125
 Db 113 YEHVUTKELDSWAKYLGRTSFDRNNWTLRLHNVQIKDMSYDCTOKKPTGSIHQ 172
 Oy 126 TLTLSYVIANFSEPEIKLAQNTGSGNLCTSKQKPPKPMFLINSTEINVDNM 185
 Db 173 TLTLSYVIANFSEPEIKLAQNTGSGNLCTSKQKPPKPMFLINSTEINVDNM 232
 Oy 186 ISQDWTLEFSINSLSPFQPMWMTVCULSTSKSPKPLFTQFSPOTWKE 245
 Db 245 ISQDWTLEFSINSLSPFQPMWMTVCULSTSKSPKPLFTQFSPOTWKE 292
 Oy 246 ITASTVALLWMLLIIVCHKQKPPQSPSTASKLRSNADRETINKLEFQIASK 305
 Db 293 ITASTVALLWMLLIIVCHKQKPPQSPSTASKLRSNADRETINKLEFQIASK 352
 Oy 306 PNAE 309
 Oy 352 PNAE 356

Db 353 PNAE 356
 RESULT 12
 US-09-441-411-15
 ; Sequence 15, Application US/09441411
 ; Publication No. US2003008342A1
 ; APPLICANT: Scholler, Nathalie B.
 ; APPLICANT: Disis, Mary L.
 ; APPLICANT: Helstrom, Ingegerd
 ; APPLICANT: Helstrom, Karl Erik
 ; TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
 ; FILE REFERENCE: 730033.409 US/09/441.411
 ; CURRENT FILING DATE: 1999-11-16
 ; NUMBER OF SEQ ID NOS: 26
 ; SEQ ID NO 15
 ; SOFTWARE: PatsEQ for Windows Version 4.0
 ; LENGTH: 303
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-09-441-411-15

Query Match
 Best Local Similarity 100.0%; Seed No. 4,6e-116; Length 303;
 Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 7 MGALHIFVTLISDAVETQVNTGYATFCPTQAQNIISLSLWVPMQOQKLV 66
 Db 1 MGALHIFVTLISDAVETQVNTGYATFCPTQAQNIISLSLWVPMQOQKLV 60
 Oy 67 BHLGTEDLSDWAKYLGRTSFDRNNWTLRLHNVQIKDMSYDCTOKKPTGSIHQ 126
 Db 61 BHLGTEDLSDWAKYLGRTSFDRNNWTLRLHNVQIKDMSYDCTOKKPTGSIHQ 120
 Oy 127 LTLSYVIANFSEPEIKLAQNTGSGNLCTSKQKPPKPMFLINSTEINVDNM 186
 Db 121 LTLSYVIANFSEPEIKLAQNTGSGNLCTSKQKPPKPMFLINSTEINVDNM 180
 Oy 187 ISQDWTLEFSINSLSPFQPMWMTVCULSTSKSPKPLFTQFSPOTWKE 246
 Db 181 ISQDWTLEFSINSLSPFQPMWMTVCULSTSKSPKPLFTQFSPOTWKE 240
 Oy 247 ITASTVALLWMLLIIVCHKQKPPQSPSTASKLRSNADRETINKLEFQIASK 306
 Db 241 ITASTVALLWMLLIIVCHKQKPPQSPSTASKLRSNADRETINKLEFQIASK 300
 Oy 307 PNAE 309
 Db 301 PNAE 303

RESULT 13
 US-09-441-411-20
 ; Sequence 20, Application US/09441411
 ; Publication No. US2003008342A1
 ; GENERAL INFORMATION: Scholler, Nathalie B.
 ; APPLICANT: Disis, Mary L.
 ; APPLICANT: Helstrom, Ingegerd
 ; APPLICANT: Helstrom, Karl Erik
 ; TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
 ; FILE REFERENCE: 730033.409
 ; CURRENT APPLICATION NUMBER: US/09/441.411
 ; CURRENT FILING DATE: 1999-11-16
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: PatsEQ for Windows Version 4.0
 ; LENGTH: 303
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-09-441-411-20

```

Query Match      97.7k; Score 1562; DB 9; Length 303;
Best Local Similarity 100.0k; Pred. No. 4,6e116; 0; Gaps 0;
Matches 303; Conservative 0; Mismatches 0;

Qy 7 MGALITPVLLISDAVSVEVNTFNGTAYLCPTTAQNSLSLSLVFWQDQVLY 66
Dy 1 MGALITPVLLISDAVSVEVNTFNGTAYLCPTTAQNSLSLSLVFWQDQVLY 60

Qy 67 ENYLGTEKLSVNAKYLGRFSNNRNLALHNVGILKMGSDCTQKPKPTSLILQQT 126
Dy 61 ENYLGTEKLSVNAKYLGRFSNNRNLALHNVGILKMGSDCTQKPKPTSLILQQT 120

Qy 127 ITLSLVINFSEETKLAQNTGNSGINTCTSCQKPKPKMFLITNSYNGNMI 186
Dy 121 ITLSLVINFSEETKLAQNTGNSGINTCTSCQKPKPKMFLITNSYNGNMI 180

Qy 187 SQNVPLFETLSNLSGLSPDSQVHMTVCVLTGSKGKSPKPYLTNSYNGNMI 246
Dy 181 SQNVPLFETLSNLSGLSPDSQVHMTVCVLTGSKGKSPKPYLTNSYNGNMI 240

Qy 247 TASTVALLMGLLITVCHKPKQPSRSTASKLERSHDAUTETNLKLEPQANAP 306
Dy 241 TASTVALLMGLLITVCHKPKQPSRSTASKLERSHDAUTETNLKLEPQANAP 300

Qy 307 ME 309
Dy 307 ME 309

Qy 301 ME 303
Dy 301 ME 303

RESULT 14
Sequence 4, Application US/08592711
Patent No. US2020119214A1
APPLICANT: Juno, Carl H.
APPLICANT: Thompson, Craig B.
APPLICANT: Nabel, Gary G.
APPLICANT: Remmett, Paul D.
TITLE OF INVENTION: Methods for Selectively Stimulating Proliferation Of T-Cells
CORRESPONDENCE ADDRESS:
ADDRESSER: LAHIVE & COCKFIELD
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0. Version #1.25
CURRENT APPLICATION DATA: US/08/592,711
FILING DATE: 26-JAN-1996
PRIOR APPLICATION DATA: US 08/581,616
FILING DATE: 4-MAY-1995
APPLICATION NUMBER: US 08/03,253
PUBLICATION NUMBER: US 5,800,189
APPLICATION NUMBER: US 08/583,944
FILING DATE: 3-JUNE-1994
APPLICATION NUMBER: US 08/073,223
APPLICATION NUMBER: US 08/200,947
FILING DATE: 23-FEB-1994
APPLICATION NUMBER: US 08/247,505
FILING DATE: 23-MAY-1994
APPLICATION NUMBER: US 08/584,866

```

```

FILING DATE: 7-APR-1992
APPLICATION NUMBER: US 09/218,155
FILING DATE: 25-MAR-1994
APPLICATION NUMBER: US 07/664,407
FILING DATE: 7-APR-1992 07/664,407
APPLICATION NUMBER: US 07/902,467
FILING DATE: 26-JUNE-1992 07/902,467
FILING DATE: 23-NOV-1988 07/275,433
ATTORNEY/AGENT INFORMATION:
FIRM NAME: BAKER, BAKER & BAKER
REGISTRATION NUMBER: 16,207
REFERENCE/DOCKET NUMBER: RPI-002CP4
TELEPHONE: (617) 237-5941
TELEFAX: (617) 237-5941
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE LENGTH: 329 amino acids
TYPE: amino acid
MOLECULE TYPE: Protein
US-08-592-711-4
Query Match      46.5k; Score 743.5; DB 8; Length 329;
Best Local Similarity 51.5k; Pred. No. 1,8e-81;
Matches 158; Conservative 45; Mismatches 91; Indels 13; Gaps 5;

Qy 1 MDPKCTMGALITPVLLISDAVSVEVNTFNGTAYLCPTTAQNSLSLSLVFWQD 60
Dy 1 MDPKCTMGALITPVLLISDAVSVEVNTFNGTAYLCPTTAQNSLSLSLVFWQD 60

Qy 61 QGLVLYHVLGTEKLSVNAKYLGRFSNNRNLALHNVGILKMGSDCTQKPKPTGS 120
Dy 61 ENYLGTEKLSVNAKYLGRFSNNRNLALHNVGILKMGSDCTQKPKPTGS 120

Qy 121 ILQQTITLSLVINFSEETKLAQNTGNSGINTCTSCQKPKPKMFLITNSYNG 178
Dy 121 ENYLGTEKLSVNAKYLGRFSNNRNLALHNVGILKMGSDCTQKPKPTGS 180

Qy 179 EYDGNQIQDQNTVLETSNLSGLSPDSQVHMTVCVLTGSKGKSPKPYLTNSY 238
Dy 181 EYDGNQIQDQNTVLETSNLSGLSPDSQVHMTVCVLTGSKGKSPKPYLTNSY 240

Qy 239 P---QTWHTTNTVALLNG---LIVVCHKPKQSPR---SNTASKLERSDNR 289
Dy 241 PPHPIHW---ITAVLPVTCVWFCILVWKKKGRHNSVYCTNTPRESSDYNKR 298

Qy 290 ETKHPE 296
Dy 299 ETKHPE 305

RESULT 15
US-09-441-411-26
Publication No. US20201008342A1
GENERAL INFORMATION:
APPLICANT: Disis, Mary L.
APPLICANT: Hallacorn, Ingegerd
APPLICANT: Hallacorn, Ingegerd
TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
FILE REFERENCE: 710033,409
CURRENT APPLICATION NUMBER: US/09/441,411
PUBLICATION NUMBER: US 6,899,116
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSeq For Windows Version 4.0
SEQUENCE LENGTH: 329
TYPE: PRT
ORIGIN: Homo sapiens
US-09-441-411-26

```

```

Query Match      46.5%, Score 743.5, DB 9, Length 329;
Best Local Similarity 51.5%, Pred. No. 1.8e-51;
Matches 198; Conservative 45; Mismatches 91; Indels 13; Gaps 5;

Qy 1 MDRCTMGALIFVTLVLLISNVETQAVFNGTAYLPCPTQAQIISLVLVWQD 60
   |||||
Db 1 MDRCTMGALIFVTLVLLISNVETQAVFNGTAYLPCPTQAQIISLVLVWQD 60

Qy 61 QGLVLYEHYIGTIELSNVAKTIGTIFDRNMVTLRLNVYQKMGSYCTFKAKPTGS 120
   |||||
Db 61 QGLVLYEHYIGTIELSNVAKTIGTIFDRNMVTLRLNVYQKMGSYCTFKAKPTGS 120

Qy 121 ILLOQTLFELVSNVSESEFLANFNSGNSINTTQSHRSHWVFLI--TNSN 178
   |||||
Db 121 ILLOQTLFELVSNVSESEFLANFNSGNSINTTQSHRSHWVFLI--TNSN 178

Qy 179 EYGNQWISQNVTEFLSISLSLSPFGQWNVTVCVLETESKISRYLNTQEPFS 238
   |||||
Db 179 EYGNQWISQNVTEFLSISLSLSPFGQWNVTVCVLETESKISRYLNTQEPFS 238

Qy 239 P---CTWKEHTASVTLVLLNLG--LIVCHKWQSPSP---SNFASKLERSDADR 289
   |||||
Db 239 P---CTWKEHTASVTLVLLNLG--LIVCHKWQSPSP---SNFASKLERSDADR 289

Qy 290 ETNLKE 296
   |||||
Db 290 ETNLKE 305

```

Search completed: February 13, 2003, 11:39:58
 208 time - 17.7514 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

ON protein - protein search, using sw model

Run on: February 13, 2003, 11:29:49 ; Search time 12.1092 Seconds
(without alignment)
750 573 Million cell updates/sec

Title: score: US-09-425-516-23

Sequences: 1: RPTNCTGLALIFVYLLIETINKELEFQIASKNMAE 309

Scoring table: BLOSUM62

Gap: 10.0, Gapext: 0.5

Searched: 262574 seqs, 2942292 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 2000000000

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

- 1: Issued Patent:AA:1/1aa/1aa COMP pep.*
- 2: /cgn2_6/pdata/1/1aa/1aa COMP pep.*
- 3: /cgn2_6/pdata/1/1aa/1aa COMP pep.*
- 4: /cgn2_6/pdata/1/1aa/1aa COMP pep.*
- 5: /cgn2_6/pdata/1/1aa/1aa COMP pep.*
- 6: /cgn2_6/pdata/1/1aa/1aa COMP pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	1599	100.0	309	2	US-08-456-104-4
2	1599	100.0	309	4	US-08-280-7518-47
3	1599	100.0	309	4	US-08-280-7518-23
4	1599	100.0	309	4	US-08-280-7518-23
5	1599	100.0	309	4	US-08-280-7518-23
6	1599	100.0	309	4	US-08-280-7518-23
7	1599	100.0	309	5	PCT-US95-0256-21
8	1599	100.0	309	5	PCT-US95-0256-21
9	1599	100.0	309	5	PCT-US95-0256-21
10	1599	100.0	309	5	PCT-US95-0256-21
11	1599	100.0	309	5	PCT-US95-0256-21
12	1599	100.0	309	5	PCT-US95-0256-21
13	1599	100.0	309	5	PCT-US95-0256-21
14	1599	100.0	309	5	PCT-US95-0256-21
15	1599	100.0	309	5	PCT-US95-0256-21
16	1599	100.0	309	5	PCT-US95-0256-21
17	1599	100.0	309	5	PCT-US95-0256-21
18	1599	100.0	309	5	PCT-US95-0256-21
19	1599	100.0	309	5	PCT-US95-0256-21
20	1599	100.0	309	5	PCT-US95-0256-21
21	1599	100.0	309	5	PCT-US95-0256-21
22	1599	100.0	309	5	PCT-US95-0256-21
23	1599	100.0	309	5	PCT-US95-0256-21
24	1599	100.0	309	5	PCT-US95-0256-21
25	1599	100.0	309	5	PCT-US95-0256-21
26	1599	100.0	309	5	PCT-US95-0256-21
27	1599	100.0	309	5	PCT-US95-0256-21

28 260 16.3 102 3 US-08-478-1648-47
29 260 16.3 102 4 US-08-286-7518-47
30 230 14.4 45 4 US-08-205-697A-30
31 230 14.4 45 5 US-08-205-697A-30
32 230 14.4 45 5 US-08-205-697A-30
33 227.5 14.2 366 4 US-08-205-697A-17
34 227.5 14.2 366 4 US-08-205-697A-17
35 227.5 14.2 366 5 PCT-US95-0256-17
36 227.5 14.2 366 5 PCT-US95-0256-17
37 227.5 14.2 366 5 PCT-US95-0256-17
38 227.5 14.2 366 5 PCT-US95-0256-17
39 227.5 14.2 366 2 US-08-147-72-4
40 227.5 14.2 366 2 US-08-147-72-4
41 227.5 14.2 366 2 US-08-147-72-4
42 227.5 14.2 366 2 US-08-147-72-4
43 227.5 14.2 366 4 US-08-478-1648-47
44 227.5 14.2 366 4 US-08-478-1648-47
45 227.5 14.2 366 4 US-08-478-1648-47

ALIGNMENTS

RESULT 1
US-08-456-104-4
Sequence 4, Application US/08456104
Patent No. 586110
Genbank Accession: X60000
APPLICANT: Freeman, Gordon J.
APPLICANT: Nedler, Lee M.
APPLICANT: Gray, Gary S.
INVENTOR: Gray, Gary S.
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS: 8
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM: disk
OPERATING SYSTEM: IBM PC compatible
OPERATING SYSTEM: IBM PC compatible
CURRENT APPLICATION DATA: Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/456,104

PRIOR APPLICATION DATA:
CLASSIFICATION: 424
APPLICATION NUMBER: 08/101,624;
APPLICATION NUMBER: 08/109,393;
APPLICATION NUMBER: 08/109,393;
APPLICATION NUMBER: 19-AUG-1993
ATTORNEY: MORTIMER, E.
REGISTRATION NUMBER: 36,207
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-7400
INVESTOR: (617) 227-5941
SEQUENCE CHARACTERISTICS: 4;
LENGTH: 309 amino acids
TYPE: amino acid
MOLECULE TYPE: Protein
US-08-456-104-4

Query Match 100.0%; Score 1599; DB 2: Length 309;
Best Local Similarity 100.0%; Pred. No. 3.2e-139;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 M0PCCTGIALIIFVTVLLISDAVETQVFNQVAFPCPTFAQNIISISELVWQDQ 60
 Db 1 M0PCCTGIALIIFVTVLLISDAVETQVFNQVAFPCPTFAQNIISISELVWQDQ 60
 Qy 61 OXUVYEHVGTGLKLSWAKYKLGFSFNNWTLPLWVQIKMGSDTCFQKQPTGS 120
 Db 61 OXUVYEHVGTGLKLSWAKYKLGFSFNNWTLPLWVQIKMGSDTCFQKQPTGS 120
 Qy 61 OXUVYEHVGTGLKLSWAKYKLGFSFNNWTLPLWVQIKMGSDTCFQKQPTGS 120
 Db 61 OXUVYEHVGTGLKLSWAKYKLGFSFNNWTLPLWVQIKMGSDTCFQKQPTGS 120
 Qy 121 IILQUTGTELVANFSPEFKLAQNTGNSNLTUSQKQPKQKQVFLINSNEY 180
 Db 121 IILQUTGTELVANFSPEFKLAQNTGNSNLTUSQKQPKQKQVFLINSNEY 180
 Qy 121 IILQUTGTELVANFSPEFKLAQNTGNSNLTUSQKQPKQKQVFLINSNEY 180
 Db 121 IILQUTGTELVANFSPEFKLAQNTGNSNLTUSQKQPKQKQVFLINSNEY 180
 Qy 181 GDNQVIGQNVTFELISNLSISPDQVWHVTVCLTESKISSEKCLNTQFFSPQ 240
 Db 181 GDNQVIGQNVTFELISNLSISPDQVWHVTVCLTESKISSEKCLNTQFFSPQ 240
 Qy 241 TWETIASVTVALLVLLIIVCHKQKQPSRNTASKLSDQNRDQRTINJALEPQ 300
 Db 241 TWETIASVTVALLVLLIIVCHKQKQPSRNTASKLSDQNRDQRTINJALEPQ 300
 Qy 301 IASAPNNE 309
 Db 301 IASAPNNE 309

RESULT 2

US-08-479-744A-23 Application US/08479744A
 ; Sequence 2340667
 ; Patent No 6130316
 ; GENERAL INFORMATION:
 ; APPLICANT: Freeman, Gordon J.
 ; APPLICANT: Gray, Gary S.
 ; TITLE OF INVENTION: No. 6084067el CTLA4/CD28 ligands and
 ; NUMBER OF INVENTIONS: 1
 ; NUMBER OF SOURCES: 53
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LAHIVE & COCKFIELD, LLP
 ; CITY: Boston
 ; STATE: MA
 ; ZIP: 02109

COMPUTER READABLE FORM

US-08-479-744A-23 Application US/08479744A
 ; Sequence 2340667
 ; Patent No 6130316
 ; GENERAL INFORMATION:
 ; APPLICANT: Freeman, Gordon J.
 ; APPLICANT: Gray, Gary S.
 ; TITLE OF INVENTION: No. 6084067el CTLA4/CD28 ligands and
 ; NUMBER OF INVENTIONS: 1
 ; NUMBER OF SOURCES: 53
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LAHIVE & COCKFIELD, LLP
 ; CITY: Boston
 ; STATE: MA
 ; ZIP: 02109

COMPUTER TYPE: FLOPPY disk

US-08-479-744A-23 Application US/08479744A
 ; Sequence 2340667
 ; Patent No 6130316
 ; GENERAL INFORMATION:
 ; APPLICANT: Freeman, Gordon J.
 ; APPLICANT: Gray, Gary S.
 ; TITLE OF INVENTION: No. 6084067el CTLA4/CD28 ligands and
 ; NUMBER OF INVENTIONS: 1
 ; NUMBER OF SOURCES: 53
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LAHIVE & COCKFIELD, LLP
 ; CITY: Boston
 ; STATE: MA
 ; ZIP: 02109

COMPUTER: IBM PC compatible

US-08-479-744A-23 Application US/08479744A
 ; Sequence 2340667
 ; Patent No 6130316
 ; GENERAL INFORMATION:
 ; APPLICANT: Freeman, Gordon J.
 ; APPLICANT: Gray, Gary S.
 ; TITLE OF INVENTION: No. 6084067el CTLA4/CD28 ligands and
 ; NUMBER OF INVENTIONS: 1
 ; NUMBER OF SOURCES: 53
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LAHIVE & COCKFIELD, LLP
 ; CITY: Boston
 ; STATE: MA
 ; ZIP: 02109

SOFTWARE: Patent in Release #1.0, Version #1.25

US-08-479-744A-23 Application US/08479744A
 ; Sequence 2340667
 ; Patent No 6130316
 ; GENERAL INFORMATION:
 ; APPLICANT: Freeman, Gordon J.
 ; APPLICANT: Gray, Gary S.
 ; TITLE OF INVENTION: No. 6084067el CTLA4/CD28 ligands and
 ; NUMBER OF INVENTIONS: 1
 ; NUMBER OF SOURCES: 53
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LAHIVE & COCKFIELD, LLP
 ; CITY: Boston
 ; STATE: MA
 ; ZIP: 02109

US-08-479-744A-23
 ; MOLECULE TYPE: protein

Qy 1 M0PCCTGIALIIFVTVLLISDAVETQVFNQVAFPCPTFAQNIISISELVWQDQ 60
 Db 1 M0PCCTGIALIIFVTVLLISDAVETQVFNQVAFPCPTFAQNIISISELVWQDQ 60
 Qy 61 OXUVYEHVGTGLKLSWAKYKLGFSFNNWTLPLWVQIKMGSDTCFQKQPTGS 120
 Db 61 OXUVYEHVGTGLKLSWAKYKLGFSFNNWTLPLWVQIKMGSDTCFQKQPTGS 120
 Qy 61 OXUVYEHVGTGLKLSWAKYKLGFSFNNWTLPLWVQIKMGSDTCFQKQPTGS 120
 Db 61 OXUVYEHVGTGLKLSWAKYKLGFSFNNWTLPLWVQIKMGSDTCFQKQPTGS 120
 Qy 121 IILQUTGTELVANFSPEFKLAQNTGNSNLTUSQKQPKQKQVFLINSNEY 180
 Db 121 IILQUTGTELVANFSPEFKLAQNTGNSNLTUSQKQPKQKQVFLINSNEY 180
 Qy 121 IILQUTGTELVANFSPEFKLAQNTGNSNLTUSQKQPKQKQVFLINSNEY 180
 Db 121 IILQUTGTELVANFSPEFKLAQNTGNSNLTUSQKQPKQKQVFLINSNEY 180
 Qy 181 GDNQVIGQNVTFELISNLSISPDQVWHVTVCLTESKISSEKCLNTQFFSPQ 240
 Db 181 GDNQVIGQNVTFELISNLSISPDQVWHVTVCLTESKISSEKCLNTQFFSPQ 240
 Qy 241 TWETIASVTVALLVLLIIVCHKQKQPSRNTASKLSDQNRDQRTINJALEPQ 300
 Db 241 TWETIASVTVALLVLLIIVCHKQKQPSRNTASKLSDQNRDQRTINJALEPQ 300
 Qy 301 IASAPNNE 309
 Db 301 IASAPNNE 309

RESULT 3

US-08-280-757B-23
 ; Sequence 2340667
 ; Patent No 6130316
 ; GENERAL INFORMATION:
 ; APPLICANT: Freeman, Gordon J.
 ; APPLICANT: Nadler, Lee M.
 ; APPLICANT: Gray, Gary S.
 ; TITLE OF INVENTION: No. 6130316el CTLA4/CD28 ligands and
 ; NUMBER OF INVENTIONS: 1
 ; NUMBER OF SOURCES: 53
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LAHIVE & COCKFIELD, LLP
 ; CITY: Boston
 ; STATE: MA
 ; ZIP: 02109

COMPUTER TYPE: FLOPPY disk

US-08-280-757B-23
 ; Sequence 2340667
 ; Patent No 6130316
 ; GENERAL INFORMATION:
 ; APPLICANT: Freeman, Gordon J.
 ; APPLICANT: Nadler, Lee M.
 ; APPLICANT: Gray, Gary S.
 ; TITLE OF INVENTION: No. 6130316el CTLA4/CD28 ligands and
 ; NUMBER OF INVENTIONS: 1
 ; NUMBER OF SOURCES: 53
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LAHIVE & COCKFIELD, LLP
 ; CITY: Boston
 ; STATE: MA
 ; ZIP: 02109

COMPUTER: IBM PC compatible

US-08-280-757B-23
 ; Sequence 2340667
 ; Patent No 6130316
 ; GENERAL INFORMATION:
 ; APPLICANT: Freeman, Gordon J.
 ; APPLICANT: Nadler, Lee M.
 ; APPLICANT: Gray, Gary S.
 ; TITLE OF INVENTION: No. 6130316el CTLA4/CD28 ligands and
 ; NUMBER OF INVENTIONS: 1
 ; NUMBER OF SOURCES: 53
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LAHIVE & COCKFIELD, LLP
 ; CITY: Boston
 ; STATE: MA
 ; ZIP: 02109

SOFTWARE: Patent in Release #1.0, Version #1.25

US-08-280-757B-23
 ; Sequence 2340667
 ; Patent No 6130316
 ; GENERAL INFORMATION:
 ; APPLICANT: Freeman, Gordon J.
 ; APPLICANT: Nadler, Lee M.
 ; APPLICANT: Gray, Gary S.
 ; TITLE OF INVENTION: No. 6130316el CTLA4/CD28 ligands and
 ; NUMBER OF INVENTIONS: 1
 ; NUMBER OF SOURCES: 53
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LAHIVE & COCKFIELD, LLP
 ; CITY: Boston
 ; STATE: MA
 ; ZIP: 02109

APPLICATION NUMBER: US/08/280,757B

US-08-280-757B-23
 ; Sequence 2340667
 ; Patent No 6130316
 ; GENERAL INFORMATION:
 ; APPLICANT: Freeman, Gordon J.
 ; APPLICANT: Nadler, Lee M.
 ; APPLICANT: Gray, Gary S.
 ; TITLE OF INVENTION: No. 6130316el CTLA4/CD28 ligands and
 ; NUMBER OF INVENTIONS: 1
 ; NUMBER OF SOURCES: 53
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LAHIVE & COCKFIELD, LLP
 ; CITY: Boston
 ; STATE: MA
 ; ZIP: 02109

CLASSIFICATION: 435

US-08-280-757B-23
 ; Sequence 2340667
 ; Patent No 6130316
 ; GENERAL INFORMATION:
 ; APPLICANT: Freeman, Gordon J.
 ; APPLICANT: Nadler, Lee M.
 ; APPLICANT: Gray, Gary S.
 ; TITLE OF INVENTION: No. 6130316el CTLA4/CD28 ligands and
 ; NUMBER OF INVENTIONS: 1
 ; NUMBER OF SOURCES: 53
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LAHIVE & COCKFIELD, LLP
 ; CITY: Boston
 ; STATE: MA
 ; ZIP: 02109

PRIOR APPLICATION DATA: 08/01,624

US-08-280-757B-23
 ; Sequence 2340667
 ; Patent No 6130316
 ; GENERAL INFORMATION:
 ; APPLICANT: Freeman, Gordon J.
 ; APPLICANT: Nadler, Lee M.
 ; APPLICANT: Gray, Gary S.
 ; TITLE OF INVENTION: No. 6130316el CTLA4/CD28 ligands and
 ; NUMBER OF INVENTIONS: 1
 ; NUMBER OF SOURCES: 53
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LAHIVE & COCKFIELD, LLP
 ; CITY: Boston
 ; STATE: MA
 ; ZIP: 02109

ATTORNEY/AGENT INFORMATION

US-08-280-757B-23
 ; Sequence 2340667
 ; Patent No 6130316
 ; GENERAL INFORMATION:
 ; APPLICANT: Freeman, Gordon J.
 ; APPLICANT: Nadler, Lee M.
 ; APPLICANT: Gray, Gary S.
 ; TITLE OF INVENTION: No. 6130316el CTLA4/CD28 ligands and
 ; NUMBER OF INVENTIONS: 1
 ; NUMBER OF SOURCES: 53
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LAHIVE & COCKFIELD, LLP
 ; CITY: Boston
 ; STATE: MA
 ; ZIP: 02109

REFERENCE/DOCKET NUMBER: RPI-004CF2

US-08-280-757B-23
 ; Sequence 2340667
 ; Patent No 6130316
 ; GENERAL INFORMATION:
 ; APPLICANT: Freeman, Gordon J.
 ; APPLICANT: Nadler, Lee M.
 ; APPLICANT: Gray, Gary S.
 ; TITLE OF INVENTION: No. 6130316el CTLA4/CD28 ligands and
 ; NUMBER OF INVENTIONS: 1
 ; NUMBER OF SOURCES: 53
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LAHIVE & COCKFIELD, LLP
 ; CITY: Boston
 ; STATE: MA
 ; ZIP: 02109

TELEFAX: (617) 227-5941
 INFORMATION FOR SEQ ID NO: 23:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 309 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MISC. FEATURES:
 US-08-20-7578-23

Query Match 100.0% Score 1599 DB 4; Length 309;
 Best Local Similarity 100.0% Pred. No 3,2e-139;
 Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPRTGMLGILFVTVLLISADVSTQAYFNATVLCPTFAQNIISLSELVPMQD 60
 DB 1 MDPRTGMLGILFVTVLLISADVSTQAYFNATVLCPTFAQNIISLSELVPMQD 60
 QY 61 QULVYEVHGTGKLSVNYKRLGTFRDNNWTLRLHVOIKMSGYDCTQKRPPTGS 120
 DB 61 QULVYEVHGTGKLSVNYKRLGTFRDNNWTLRLHVOIKMSGYDCTQKRPPTGS 120
 QY 121 HLTQQTTELSVAFSEPEIKLAQVNTGKINLTCTSKQHPKPKKRYATLTNSTNEY 180
 DB 121 HLTQQTTELSVAFSEPEIKLAQVNTGKINLTCTSKQHPKPKKRYATLTNSTNEY 180
 QY 181 GNNQIQGQNTVEISNISLSISLSPFQVWMTYVTVLHTEKMLISKATFTQEPSPQ 240
 DB 181 GNNQIQGQNTVEISNISLSISLSPFQVWMTYVTVLHTEKMLISKATFTQEPSPQ 240
 QY 241 TWKSTASTVATVALLMLLVCHKPNQDPSSTASKLRSNADRETINLXLETPQ 300
 DB 241 TWKSTASTVATVALLMLLVCHKPNQDPSSTASKLRSNADRETINLXLETPQ 300
 QY 301 TASAPNAE 309
 DB 301 TASAPNAE 309

RESULT 4
 US-08-205-697A-21 Application US/08205697A
 Patent No. 6218510
 GENERAL INFORMATION:
 APPLICANT: Sharpe, Arlene H.
 APPLICANT: Sharpe, Arlene H.
 APPLICANT: Freeman, Gordon J.
 APPLICANT: Nadler, Lee M.
 TITLE OF INVENTION: Molecules and Uses Thereof
 NUMBER OF SEQUENCES: 61
 NUMBER OF SEQUENCES: 61
 ADDRESS: 28 State Street
 ADDRESS: 28 State Street, suite 510
 CITY: Boston
 CITY: Boston
 STATE: Massachusetts
 STATE: Massachusetts
 COUNTRY: USA
 COUNTRY: USA
 ZIP: 02109-1875
 ZIP: 02109-1875
 COMPUTER: IBM PC compatible
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/205,697A
 APPLICATION NUMBER: US/08/205,697A
 ATTORNEY/AGENT INFORMATION:
 NAME: Mandragoules, Amy E.
 NAME: Mandragoules, Amy E.
 REFERENCE/DOCKET NUMBER: 36,204-120
 REFERENCE/DOCKET NUMBER: 36,204-120
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400
 TELEPHONE: (617) 227-7400
 INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:
 LENGTH: 309 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MISC. FEATURES:
 US-08-205-697A-21

Query Match 100.0% Score 1599 DB 4; Length 309;
 Best Local Similarity 100.0% Pred. No 3,2e-139;
 Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPRTGMLGILFVTVLLISADVSTQAYFNATVLCPTFAQNIISLSELVPMQD 60
 DB 1 MDPRTGMLGILFVTVLLISADVSTQAYFNATVLCPTFAQNIISLSELVPMQD 60
 QY 61 QULVYEVHGTGKLSVNYKRLGTFRDNNWTLRLHVOIKMSGYDCTQKRPPTGS 120
 DB 61 QULVYEVHGTGKLSVNYKRLGTFRDNNWTLRLHVOIKMSGYDCTQKRPPTGS 120
 QY 121 HLTQQTTELSVAFSEPEIKLAQVNTGKINLTCTSKQHPKPKKRYATLTNSTNEY 180
 DB 121 HLTQQTTELSVAFSEPEIKLAQVNTGKINLTCTSKQHPKPKKRYATLTNSTNEY 180
 QY 181 GNNQIQGQNTVEISNISLSISLSPFQVWMTYVTVLHTEKMLISKATFTQEPSPQ 240
 DB 181 GNNQIQGQNTVEISNISLSISLSPFQVWMTYVTVLHTEKMLISKATFTQEPSPQ 240
 QY 241 TWKSTASTVATVALLMLLVCHKPNQDPSSTASKLRSNADRETINLXLETPQ 300
 DB 241 TWKSTASTVATVALLMLLVCHKPNQDPSSTASKLRSNADRETINLXLETPQ 300
 QY 301 TASAPNAE 309
 DB 301 TASAPNAE 309

RESULT 5
 US-08-205-697A-21 Application US/08703525
 Patent No. 6234660
 GENERAL INFORMATION:
 APPLICANT: Sharpe
 APPLICANT: Borriello, Francesco Paolo
 APPLICANT: Freeman, Gordon
 APPLICANT: Freeman, Gordon
 TITLE OF INVENTION: Molecules and Uses Thereof
 NUMBER OF SEQUENCES: 65
 NUMBER OF SEQUENCES: 65
 ADDRESS: 28 State Street
 ADDRESS: 28 State Street
 ADDRESS: LAHIVE & COCKFIELD
 ADDRESS: LAHIVE & COCKFIELD
 CITY: Boston
 CITY: Boston
 STATE: Massachusetts
 STATE: Massachusetts
 COUNTRY: USA
 COUNTRY: USA
 ZIP: 02109-1875
 ZIP: 02109-1875
 COMPUTER: IBM PC compatible
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/703,525
 APPLICATION NUMBER: US/08/703,525
 ATTORNEY/AGENT INFORMATION:
 NAME: Mandragoules, Amy E.
 NAME: Mandragoules, Amy E.
 REFERENCE/DOCKET NUMBER: 36,204-120
 REFERENCE/DOCKET NUMBER: 36,204-120
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400
 TELEPHONE: (617) 227-7400
 INFORMATION FOR SEQ ID NO: 21:


```

Db 121 11QQQTVELTSVIANFSEPR1KLAQVTVNGSGLNLTSCQKQFPRKMYFL1NSTYNN 180
Oy 181 GNNQIQDQNTVELTSVINSLSLFFQPGQVMMHTVVCVLETESKMSKSPFNTPQPYWK 244
Db 181 GNNQIQDQNTVELTSVINSLSLFFQPGQVMMHTVVCVLETESKMSKSPFNTPQPYWK 249
Oy 245 BITASVTAVTALLVMULLITVCHKPKQSPRSNTASKLSDSNADRTIKLEBPQASA 304
Db 245 BITASVTAVTALLVMULLITVCHKPKQSPRSNTASKLSDSNADRTIKLEBPQASA 309
Oy 241 TYKKE1TASVTAVTALLVMULLITVCHKPKQSPRSNTASKLSDSNADRTIKLEBPQ 300
Db 241 TYKKE1TASVTAVTALLVMULLITVCHKPKQSPRSNTASKLSDSNADRTIKLEBPQ 309
Oy 301 IASGNPAE 309
Db 301 IASGNPAE 309
Oy 301 IASGNPAE 309
Db 301 IASGNPAE 309

RESULT 8
US-08-205-697A-13
: Sequence 13, Application US/08205697A
: Match No. 1
: GENERAL INFORMATION:
: APPLICANT: Sharpe, Arlene H.
: APPLICANT: Borriello, Francescapolo
: APPLICANT: Franzen, Gordon
: APPLICANT: Nadler, Lee M.
: TITLE OF INVENTION: No. 6218510el, Forms of T Cell Costimulatory Molecules
: NUMBER OF SEQUENCES: 65
: NUMBER OF SEQUENCES: 65
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: LO JAHNVE & COCKFIELD
: STREET: 28 State Street, Suite 510
: CITY: Boston
: STATE: Massachusetts
: ZIP: 02109-1875
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: ASCII Text
: APPLICATION NUMBER: US/08/205,697A
: FILING DATE: 02-Mar-1994
: PRIORITY/AGENT INFORMATION:
: REFERENCE/DOCKET NUMBER: BM-120
: TELEPHONE: (617) 227-5541
: TELEFAX: (617) 227-5541
: INQUIRY CONTACT: SEC 13:
: SEQUENCE CHARACTERISTICS 13:
: TYPE: amino acid
: MOLECULE TYPE: Protein
US-08-205-697A-13

Query Match
Best Local Similarity 100.0%, Pred. No. 4.3e-137,
Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 CTGMLAL1PVTYLLISDAVSVEYQVNTGYALPCPTFAKQNIISLELVFMQDQKLV 64
Db 10 CTGMLAL1PVTYLLISDAVSVEYQVNTGYALPCPTFAKQNIISLELVFMQDQKLV 69
Oy 65 LYBVTZLTGKLSVANKYKLTGRSDRNNTVLRJNVQIKNGSDYCFI QKQPTGSI11Q 124
Db 70 LYBVTZLTGKLSVANKYKLTGRSDRNNTVLRJNVQIKNGSDYCFI QKQPTGSI11Q 129
Oy 125 OTTLETSVIANFSEPR1KLAQVTVNGSGLNLTSCQKQFPRKMYFL1NSTYNN 184
Db 130 OTTLETSVIANFSEPR1KLAQVTVNGSGLNLTSCQKQFPRKMYFL1NSTYNN 189

```

```

Oy 185 QIQDQNTVELTSVINSLSLFFQPGQVMMHTVVCVLETESKMSKSPFNTPQPYWK 244
Db 190 QIQDQNTVELTSVINSLSLFFQPGQVMMHTVVCVLETESKMSKSPFNTPQPYWK 249
Oy 245 BITASVTAVTALLVMULLITVCHKPKQSPRSNTASKLSDSNADRTIKLEBPQASA 304
Db 250 BITASVTAVTALLVMULLITVCHKPKQSPRSNTASKLSDSNADRTIKLEBPQASA 309
Oy 305 KPANE 309
Db 310 KPANE 314

RESULT 9
US-08-702-525-13
: Sequence 13, Application US/08702525
: Match No. 1
: GENERAL INFORMATION:
: APPLICANT: Sharpe, Arlene H.
: APPLICANT: Borriello, Francescapolo
: APPLICANT: Franzen, Gordon
: APPLICANT: Nadler, Lee
: TITLE OF INVENTION: No. 6214660el, Forms of T Cell Costimulatory
: NUMBER OF SEQUENCES: 65
: NUMBER OF SEQUENCES: 65
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: LO JAHNVE & COCKFIELD
: STREET: 28 State Street
: CITY: Boston
: STATE: Massachusetts
: ZIP: 02109-1875
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: ASCII Text
: APPLICATION NUMBER: US/08/702,525
: FILING DATE: 02-Mar-1994
: PRIORITY/AGENT INFORMATION:
: REFERENCE/DOCKET NUMBER: BM-120CDSU
: TELEPHONE: (617) 227-7400
: TELEFAX: (617) 227-5941
: INQUIRY CONTACT: SEC 13:
: SEQUENCE CHARACTERISTICS 13:
: TYPE: amino acid
: MOLECULE TYPE: protein
US-08-702-525-13

Query Match
Best Local Similarity 100.0%, Pred. No. 4.3e-137,
Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 CTGMLAL1PVTYLLISDAVSVEYQVNTGYALPCPTFAKQNIISLELVFMQDQKLV 64
Db 10 CTGMLAL1PVTYLLISDAVSVEYQVNTGYALPCPTFAKQNIISLELVFMQDQKLV 69
Oy 65 LYBVTZLTGKLSVANKYKLTGRSDRNNTVLRJNVQIKNGSDYCFI QKQPTGSI11Q 124
Db 70 LYBVTZLTGKLSVANKYKLTGRSDRNNTVLRJNVQIKNGSDYCFI QKQPTGSI11Q 129
Oy 125 OTTLETSVIANFSEPR1KLAQVTVNGSGLNLTSCQKQFPRKMYFL1NSTYNN 184

```

```

Db 130 OTTLESTVIANFSEPEIKLAQNTVNSGIALCTCKGKHQKPMKWLFTNTEYNDGM 189
Oy 185 QICQNVLTLSISNSLSFPGQVHNTVVCVLETSMKISKPJFTTFFSPOTYWK 244
Oy 190 QICQNVLTLSISNSLSFPGQVHNTVVCVLETSMKISKPJFTTFFSPOTYWK 249
Oy 245 ETTSQVTVALLVLLIIVCHKPKQSPRNTASKLERUSNADRETINKELEPOJAS 304
Oy 250 ETTSQVTVALLVLLIIVCHKPKQSPRNTASKLERUSNADRETINKELEPOJAS 309
Oy 305 KPMAS 309
Oy 310 KPMAS 314
|||||
RESULT 10
PCT-US95-02576-13
GENERAL INFORMATION:
PCT/US9502576
APPLICANT:
TITLE OF INVENTION: Novel Forms of T Cell Costimulatory Molecules
TITLE OF INVENTION: Polynucleotides Encoding Members of the Human B
Lymphocyte Activation Antigen B-7 Family and
METHODS OF USING THE SAME
FILE REFERENCE: 15946-562 CUBA-42
CURRENT APPLICATION NUMBER: US/09/651,200
PRIORITY CLAIM: YES
PRIORITY APPLICATION NUMBER: 60/152383
PRIORITY FILING DATE: 1999-09-03
PRIORITY APPLICATION NUMBER: 12-521,47309
PRIORITY FILING DATE: 2000-02-18
PRIORITY APPLICATION NUMBER: 60/183578
PRIORITY FILING DATE: 2000-02-18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 23
SEQUENCE:
TYPE: PRT
ORGANISM: Mus musculus
US-09-451-200-23
Query Match
Best Local Similarity 100.0%; Pred. No. 4e-136; Indels 0, Gaps 0,
Matches 305, Conservative 0, Mismatches 0
Oy 7 MGALILFTVLISADVETQVNTATLCPPTQAQISLSLWVPMQDQKLV 66
Oy 1 MGALILFTVLISADVETQVNTATLCPPTQAQISLSLWVPMQDQKLV 60
Db 61 EHYLGTLEKLSVNARYKLTGSPDNNTLRLNVAIKMKSCTCTOKPFTSILQOT 126
Oy 67 EHYLGTLEKLSVNARYKLTGSPDNNTLRLNVAIKMKSCTCTOKPFTSILQOT 120
Oy 127 LTELSTVIANFSEPEIKLAQNTVNSGIALCTCKGKHQKPMKWLFTNTEYNDGM 186
Oy 121 LTELSTVIANFSEPEIKLAQNTVNSGIALCTCKGKHQKPMKWLFTNTEYNDGM 180
Oy 187 SQDNVLTLSISNSLSFPGQVHNTVVCVLETSMKISKPJFTTFFSPOTYWK 240
Oy 181 SQDNVLTLSISNSLSFPGQVHNTVVCVLETSMKISKPJFTTFFSPOTYWK 246
Oy 247 TASTVTVALLVLLIIVCHKPKQSPRNTASKLERUSNADRETINKELEPOJAS 306
Oy 241 TASTVTVALLVLLIIVCHKPKQSPRNTASKLERUSNADRETINKELEPOJAS 300
Oy 307 NAE 309
Oy 301 NAE 303
|||||
RESULT 12
PCT-US95-02576-13
GENERAL INFORMATION:
PCT/US9502576
APPLICANT:
TITLE OF INVENTION: Novel Forms of T Cell Costimulatory Molecules
TITLE OF INVENTION: Polynucleotides Encoding Members of the Human B
Lymphocyte Activation Antigen B-7 Family and
METHODS OF USING THE SAME
FILE REFERENCE: 15946-562 CUBA-42
CURRENT APPLICATION NUMBER: US/09/651,200
PRIORITY CLAIM: YES
PRIORITY APPLICATION NUMBER: 60/152383
PRIORITY FILING DATE: 1999-09-03
PRIORITY APPLICATION NUMBER: 12-521,47309
PRIORITY FILING DATE: 2000-02-18
PRIORITY APPLICATION NUMBER: 60/183578
PRIORITY FILING DATE: 2000-02-18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 23
SEQUENCE:
TYPE: PRT
ORGANISM: Mus musculus
US-09-451-200-23
Query Match
Best Local Similarity 100.0%; Pred. No. 4.3e-137; Indels 0, Gaps 0,
Matches 305, Conservative 0, Mismatches 0
Oy 5 CTGHALILFTVLISADVETQVNTATLCPPTQAQISLSLWVPMQDQKLV 64
Oy 1 CTGHALILFTVLISADVETQVNTATLCPPTQAQISLSLWVPMQDQKLV 69
Oy 65 EHYLGTLEKLSVNARYKLTGSPDNNTLRLNVAIKMKSCTCTOKPFTSILQOT 124
Oy 70 EHYLGTLEKLSVNARYKLTGSPDNNTLRLNVAIKMKSCTCTOKPFTSILQOT 129
Oy 125 OTTLESTVIANFSEPEIKLAQNTVNSGIALCTCKGKHQKPMKWLFTNTEYNDGM 184
Oy 121 OTTLESTVIANFSEPEIKLAQNTVNSGIALCTCKGKHQKPMKWLFTNTEYNDGM 189
Oy 130 OTTLESTVIANFSEPEIKLAQNTVNSGIALCTCKGKHQKPMKWLFTNTEYNDGM 189
Oy 185 QICQNVLTLSISNSLSFPGQVHNTVVCVLETSMKISKPJFTTFFSPOTYWK 244

```

```

Db 190 QICQNVLTLSISNSLSFPGQVHNTVVCVLETSMKISKPJFTTFFSPOTYWK 249
Oy 245 ETTSQVTVALLVLLIIVCHKPKQSPRNTASKLERUSNADRETINKELEPOJAS 304
Oy 250 ETTSQVTVALLVLLIIVCHKPKQSPRNTASKLERUSNADRETINKELEPOJAS 309
Oy 305 KPMAS 309
Oy 310 KPMAS 314
|||||
RESULT 11
PCT-US95-02576-13
GENERAL INFORMATION:
PCT/US9502576
APPLICANT:
TITLE OF INVENTION: Novel Forms of T Cell Costimulatory Molecules
TITLE OF INVENTION: Polynucleotides Encoding Members of the Human B
Lymphocyte Activation Antigen B-7 Family and
METHODS OF USING THE SAME
FILE REFERENCE: 15946-562 CUBA-42
CURRENT APPLICATION NUMBER: US/09/651,200
PRIORITY CLAIM: YES
PRIORITY APPLICATION NUMBER: 60/152383
PRIORITY FILING DATE: 1999-09-03
PRIORITY APPLICATION NUMBER: 12-521,47309
PRIORITY FILING DATE: 2000-02-18
PRIORITY APPLICATION NUMBER: 60/183578
PRIORITY FILING DATE: 2000-02-18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 23
SEQUENCE:
TYPE: PRT
ORGANISM: Mus musculus
US-09-451-200-23
Query Match
Best Local Similarity 100.0%; Pred. No. 4e-136; Indels 0, Gaps 0,
Matches 305, Conservative 0, Mismatches 0
Oy 7 MGALILFTVLISADVETQVNTATLCPPTQAQISLSLWVPMQDQKLV 66
Oy 1 MGALILFTVLISADVETQVNTATLCPPTQAQISLSLWVPMQDQKLV 60
Db 61 EHYLGTLEKLSVNARYKLTGSPDNNTLRLNVAIKMKSCTCTOKPFTSILQOT 126
Oy 67 EHYLGTLEKLSVNARYKLTGSPDNNTLRLNVAIKMKSCTCTOKPFTSILQOT 120
Oy 127 LTELSTVIANFSEPEIKLAQNTVNSGIALCTCKGKHQKPMKWLFTNTEYNDGM 186
Oy 121 LTELSTVIANFSEPEIKLAQNTVNSGIALCTCKGKHQKPMKWLFTNTEYNDGM 180
Oy 187 SQDNVLTLSISNSLSFPGQVHNTVVCVLETSMKISKPJFTTFFSPOTYWK 240
Oy 181 SQDNVLTLSISNSLSFPGQVHNTVVCVLETSMKISKPJFTTFFSPOTYWK 246
Oy 247 TASTVTVALLVLLIIVCHKPKQSPRNTASKLERUSNADRETINKELEPOJAS 306
Oy 241 TASTVTVALLVLLIIVCHKPKQSPRNTASKLERUSNADRETINKELEPOJAS 300
Oy 307 NAE 309
Oy 301 NAE 303
|||||
RESULT 12
PCT-US95-02576-13
GENERAL INFORMATION:
PCT/US9502576
APPLICANT:
TITLE OF INVENTION: Novel Forms of T Cell Costimulatory Molecules
TITLE OF INVENTION: Polynucleotides Encoding Members of the Human B
Lymphocyte Activation Antigen B-7 Family and
METHODS OF USING THE SAME
FILE REFERENCE: 15946-562 CUBA-42
CURRENT APPLICATION NUMBER: US/09/651,200
PRIORITY CLAIM: YES
PRIORITY APPLICATION NUMBER: 60/152383
PRIORITY FILING DATE: 1999-09-03
PRIORITY APPLICATION NUMBER: 12-521,47309
PRIORITY FILING DATE: 2000-02-18
PRIORITY APPLICATION NUMBER: 60/183578
PRIORITY FILING DATE: 2000-02-18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 23
SEQUENCE:
TYPE: PRT
ORGANISM: Mus musculus
US-09-451-200-23
Query Match
Best Local Similarity 100.0%; Pred. No. 4.3e-137; Indels 0, Gaps 0,
Matches 305, Conservative 0, Mismatches 0
Oy 5 CTGHALILFTVLISADVETQVNTATLCPPTQAQISLSLWVPMQDQKLV 64
Oy 1 CTGHALILFTVLISADVETQVNTATLCPPTQAQISLSLWVPMQDQKLV 69
Oy 65 EHYLGTLEKLSVNARYKLTGSPDNNTLRLNVAIKMKSCTCTOKPFTSILQOT 124
Oy 70 EHYLGTLEKLSVNARYKLTGSPDNNTLRLNVAIKMKSCTCTOKPFTSILQOT 129
Oy 125 OTTLESTVIANFSEPEIKLAQNTVNSGIALCTCKGKHQKPMKWLFTNTEYNDGM 184
Oy 121 OTTLESTVIANFSEPEIKLAQNTVNSGIALCTCKGKHQKPMKWLFTNTEYNDGM 189
Oy 130 OTTLESTVIANFSEPEIKLAQNTVNSGIALCTCKGKHQKPMKWLFTNTEYNDGM 189
Oy 185 QICQNVLTLSISNSLSFPGQVHNTVVCVLETSMKISKPJFTTFFSPOTYWK 244

```

1 APPLICANT: Nadler, Lee M.
 2 APPLICANT: Gray, Gary S.
 3 NUMBER OF SEQUENCES: 8
 4 CORRESPONDENCE ADDRESSES:
 5 ADDRESSEE: LATIVE & COCKFIELD
 6 ADDRESSEE: 60 State Street, Suite 510
 7 CITY: Boston
 8 STATE: Massachusetts
 9 ZIP: 02109
 10
 11 COMPUTER READABLE FORM:
 12 COMPUTER: IBM PC compatible
 13 OPERATING SYSTEM: PC-DOS/MS-DOS
 14 SOFTWARE: PatentIn Release #1.0, Version #1.25
 15 CLIENT: PatentIn Release #1.0, Version #1.25
 16 APPLICATION NUMBER: US/08/456,104
 17 FILING DATE: 09/10/1993
 18 PRIORITY DATE: 09/10/1993
 19 PRIOR APPLICATION DATA:
 20 APPLICATION NUMBER: 09/101,624;
 21 FILING DATE: 26-JUL-1993;
 22 PRIORITY DATE: 19-AUG-1993
 23 APPLICATION NUMBER: 19-AUG-1993
 24
 25 ATTORNEY/AGENT INFORMATION:
 26 REGISTRATION NUMBER: 36,207
 27 REFERENCE/DOCKET NUMBER: RPI-008
 28 TELEPHONE: (617) 227-5941
 29 TELEFAX: (617) 227-5941
 30 INFORMATION FOR SEQ ID NO: 1:
 31 TYPE: amino acid
 32 LENGTH: 319 amino acids
 33 MOLECULES TYPE: linear
 34 US-08-456-104-2

Query Match 46.5% Score 743.5 DB 2; Length 329;
Best Local Similarity 51.5% Pred No. 1,7660;

Matches 158; Conservative 45; Mismatches 91; Indels 13; Gaps 5;

Oy 1 MDPCCTGGLALIFVYLLSDANVETQVNGTAVLPCPTTAAKNSLSLVLVFWQD 60
 Oy 1 MDPCCTGGLALIFVYLLSDANVETQVNGTAVLPCPTTAAKNSLSLVLVFWQD 60
 Oy 61 QKVLVYVETGLDLSVNAKYLQTSFORNWTLLRHVQIKMSGYCTCKEPTGTS 120
 Oy 61 ENLVYVETGLDLSVNAKYLQTSFORNWTLLRHVQIKMSGYCTCKEPTGTS 120
 Oy 121 LIQQTTELSVNAKYLQTSFORNWTLLRHVQIKMSGYCTCKEPTGTS 178
 Oy 121 LIQQTTELSVNAKYLQTSFORNWTLLRHVQIKMSGYCTCKEPTGTS 178
 Oy 121 LIQQTTELSVNAKYLQTSFORNWTLLRHVQIKMSGYCTCKEPTGTS 178
 Oy 179 EYGMNDQSDNTELSVNAKYLQTSFORNWTLLRHVQIKMSGYCTCKEPTGTS 180
 Oy 181 EYGMNDQSDNTELSVNAKYLQTSFORNWTLLRHVQIKMSGYCTCKEPTGTS 218
 Oy 218 EYGMNDQSDNTELSVNAKYLQTSFORNWTLLRHVQIKMSGYCTCKEPTGTS 240
 Oy 240 EYGMNDQSDNTELSVNAKYLQTSFORNWTLLRHVQIKMSGYCTCKEPTGTS 240
 Oy 239 P---OTWTKETVYVALLVM---LIIVCKKPNQPRP---SNTSKLQSDNAR 289
 Oy 241 PPDHPIH--ITAVLPVLCVWFLCLLKKKKKPNSTKGTNMBREBQTKR 298
 Oy 290 ETKHPE 296
 Oy 299 ETKHPE 305

RESULT 13
 US-08-456-104-2
 ; Sequence 2, Application US/08/01,624
 ; Patent No. 5542607

1 GENERAL INFORMATION:
 2 APPLICANT: Freeman, Gordon J.
 3 APPLICANT: Nadler, Lee M.
 4 TITLE OF INVENTION: CTLA4/CD28 Ligande and
 5 ADDRESSEE: LATIVE & COCKFIELD
 6 ADDRESSEE: 60 State Street, Suite 510
 7 CITY: Boston
 8 STATE: Massachusetts
 9 ZIP: 02109
 10
 11 COMPUTER READABLE FORM:
 12 COMPUTER: IBM PC compatible
 13 OPERATING SYSTEM: PC-DOS/MS-DOS
 14 SOFTWARE: PatentIn Release #1.0, Version #1.25
 15 CLIENT: PatentIn Release #1.0, Version #1.25
 16 APPLICATION NUMBER: US/08/101,624
 17 FILING DATE: 09/10/1993
 18 PRIORITY DATE: 09/10/1993
 19 PRIOR APPLICATION DATA:
 20 APPLICATION NUMBER:
 21 FILING DATE:
 22 PRIORITY DATE:
 23 APPLICATION NUMBER:
 24
 25 ATTORNEY/AGENT INFORMATION:
 26 REGISTRATION NUMBER: 36,207
 27 REFERENCE/DOCKET NUMBER: RPI-004
 28 TELEPHONE: (617) 227-5941
 29 TELEFAX: (617) 227-5941
 30 INFORMATION FOR SEQ ID NO: 2:
 31 TYPE: amino acid
 32 LENGTH: 319 amino acids
 33 MOLECULES TYPE: linear
 34 US-08-101-624-2

Query Match 46.5% Score 743.5 DB 2; Length 329;
Best Local Similarity 51.5% Pred No. 1,7660;

Matches 158; Conservative 45; Mismatches 91; Indels 13; Gaps 5;

Oy 1 MDPCCTGGLALIFVYLLSDANVETQVNGTAVLPCPTTAAKNSLSLVLVFWQD 60
 Oy 1 MDPCCTGGLALIFVYLLSDANVETQVNGTAVLPCPTTAAKNSLSLVLVFWQD 60
 Oy 61 QKVLVYVETGLDLSVNAKYLQTSFORNWTLLRHVQIKMSGYCTCKEPTGTS 120
 Oy 61 ENLVYVETGLDLSVNAKYLQTSFORNWTLLRHVQIKMSGYCTCKEPTGTS 120
 Oy 121 LIQQTTELSVNAKYLQTSFORNWTLLRHVQIKMSGYCTCKEPTGTS 178
 Oy 121 LIQQTTELSVNAKYLQTSFORNWTLLRHVQIKMSGYCTCKEPTGTS 178
 Oy 121 LIQQTTELSVNAKYLQTSFORNWTLLRHVQIKMSGYCTCKEPTGTS 178
 Oy 179 EYGMNDQSDNTELSVNAKYLQTSFORNWTLLRHVQIKMSGYCTCKEPTGTS 180
 Oy 181 EYGMNDQSDNTELSVNAKYLQTSFORNWTLLRHVQIKMSGYCTCKEPTGTS 218
 Oy 218 EYGMNDQSDNTELSVNAKYLQTSFORNWTLLRHVQIKMSGYCTCKEPTGTS 240
 Oy 239 P---OTWTKETVYVALLVM---LIIVCKKPNQPRP---SNTSKLQSDNAR 289
 Oy 241 PPDHPIH--ITAVLPVLCVWFLCLLKKKKKPNSTKGTNMBREBQTKR 298
 Oy 290 ETKHPE 296
 Oy 299 ETKHPE 305

RESULT 14
 US-08-479-144A-2
 ; Sequence 2, Application US/08479144A

```

Patent No.: 6084047
CLASSIFICATION:
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
TITLE OF INVENTION: No. 60840761 CTLA/CD28 Ligands and
NUMBER OF SEQUENCES: 55
COUNTRY: USA
ADDRESSES: LAHVE & COCKFIELD LLP
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: 08/479,744A
FILING DATE: June 7, 1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 08/280,757
FILING DATE: 26-JUL-1994
APPLICATION NUMBER: 08/109,393
FILING DATE: 26-JUL-1993
APPLICATION NUMBER: 08/101,624
FILING DATE: 26-JUL-1993
FILING DATE: 3-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mandreghoure, Amy B.
REFERENCE/DOCKET NUMBER: RPI 004CT3
TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS
TYPE: amino acid
TOPOLOGY: linear
MOLWGLOT: protein
US-08-479-744A-2
46.58; Scope 743.5; Db 3; Length 339;
Query Match
Similarity 51.5%; Pred. No. 1,7e-60;
Matches 158; Conservative 45; Mismatches 91; Indels 13; Gaps 5;
QY 1 MDPCTGALALIFVTLVLSISVAVTQVNGTAVLPCTPAQKQISLSLVFPMQD 60
Db 1 MDPCTGALALIFVTLVLSISVAVTQVNGTAVLPCTPAQKQISLSLVFPMQD 60
QY 61 OLVLVYHGTGKLSVNSVNAKPLQATFNTADLPQFANQKQISLSLVFPMQD 120
Db 61 OLVLVYHGTGKLSVNSVNAKPLQATFNTADLPQFANQKQISLSLVFPMQD 120
QY 61 ENLVAVYVQKRFVSHKMKRISFDSVILKQALQKQVLCILHKKPTQ 120
Db 61 ENLVAVYVQKRFVSHKMKRISFDSVILKQALQKQVLCILHKKPTQ 120
QY 121 ILIQQLTVELSVANFSEPIKLAQVNGSINTCTSKQHPKPMYFL--TNSTN 178
Db 121 ILIQQLTVELSVANFSEPIKLAQVNGSINTCTSKQHPKPMYFL--TNSTN 178
QY 131 IETQKMSVLSANFQPELVFNSTVNTVNYINLCSSVHVSFAMSVLTNSTI 180
Db 131 IETQKMSVLSANFQPELVFNSTVNTVNYINLCSSVHVSFAMSVLTNSTI 180
QY 179 EYQKMSQDQNTVELFISNISLSFPFQVHVMVTVCVLTETMSISKPLNFQEPS 218
Db 179 EYQKMSQDQNTVELFISNISLSFPFQVHVMVTVCVLTETMSISKPLNFQEPS 218
QY 181 EYQKMSQDQNTVELFISNISLSFPFQVHVMVTVCVLTETMSISKPLNFQEPS 240
Db 181 EYQKMSQDQNTVELFISNISLSFPFQVHVMVTVCVLTETMSISKPLNFQEPS 240
QY 239 P--QTVKMTFASVTVALLAM--ILVCKVNMQKQRP---SNFASVSRDNAR 289
Db 241 PPHHLPN--ITAVLPVILCWVFLILMKKKKRRPNSKYCQNTMESEBQTKR 298
QY 290 ETKNMX 296
Db 290 ETKNMX 296

```

```

DB 299 EKHIPe 305
RESULT 15
US-08-280-757B-2
Sequence 2: Application US/08280/757B
GENERAL INFORMATION:
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
APPLICANT: Gray, Gary S.
APPLICANT: Greenfield, Edward
TITLE OF INVENTION: CTLA/CD28 Ligands and
NUMBER OF SEQUENCES: 53
COMPLEMENT ADDRESS: COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/280,757B
FILING DATE: 26-JUL-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/101,624
FILING DATE: 26-JUL-1993
APPLICATION NUMBER: 08/109,393
FILING DATE: 19-AUG-1993
FILING DATE: 3-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mandreghoure, Amy B.
REFERENCE/DOCKET NUMBER: RPI-004CT2
TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS
TYPE: amino acid
TOPOLOGY: linear
MOLWGLOT: protein
US-08-280-757B-2
46.58; Scope 743.5; Db 4; Length 339;
Query Match
Similarity 51.5%; Pred. No. 1,7e-60;
Matches 158; Conservative 45; Mismatches 91; Indels 13; Gaps 5;
QY 1 MDPCTGALALIFVTLVLSISVAVTQVNGTAVLPCTPAQKQISLSLVFPMQD 60
Db 1 MDPCTGALALIFVTLVLSISVAVTQVNGTAVLPCTPAQKQISLSLVFPMQD 60
QY 61 OLVLVYHGTGKLSVNSVNAKPLQATFNTADLPQFANQKQISLSLVFPMQD 120
Db 61 OLVLVYHGTGKLSVNSVNAKPLQATFNTADLPQFANQKQISLSLVFPMQD 120
QY 121 ILIQQLTVELSVANFSEPIKLAQVNGSINTCTSKQHPKPMYFL--TNSTN 178
Db 121 ILIQQLTVELSVANFSEPIKLAQVNGSINTCTSKQHPKPMYFL--TNSTN 178
QY 131 IETQKMSVLSANFQPELVFNSTVNTVNYINLCSSVHVSFAMSVLTNSTI 180
Db 131 IETQKMSVLSANFQPELVFNSTVNTVNYINLCSSVHVSFAMSVLTNSTI 180
QY 179 EYQKMSQDQNTVELFISNISLSFPFQVHVMVTVCVLTETMSISKPLNFQEPS 238
Db 179 EYQKMSQDQNTVELFISNISLSFPFQVHVMVTVCVLTETMSISKPLNFQEPS 238
QY 181 EYQKMSQDQNTVELFISNISLSFPFQVHVMVTVCVLTETMSISKPLNFQEPS 240
Db 181 EYQKMSQDQNTVELFISNISLSFPFQVHVMVTVCVLTETMSISKPLNFQEPS 240

```

Qy 239 P---OTWKETASVTVALUML--IIIVCHQPNQSP---SNTASKLEROSNAUR 289
 Db 241 PPDH1PW--TANLPTV1ICWVFL1LWKKKKKPPNSYKGTINRESEOTJKN 288
 Qy 290 PTHUKE 296
 Db 299 EXH1PPE 305

Search completed: February 13, 2003, 11:33:52
 Job time : 13.1082 secs

